

24350

U.S. DEPARTMENT OF COMMERCE
Patent and Trademark Office

SEARCH REQUEST FORM

Requestor's

Name:

GAMBEL

Serial

Number:

08/487283

Date:

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Phone:

303-3997

Art Unit:

1644

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

9/6-9/6/00-

SEQ + SEQ INTERFERENCE SEARCH

abnng 1 9/6-494-458

9/7-431-435

343-394

9/9-350-354

9/10-297-301

9/11-250-254

9/12-195-199

(25-29)

SEQ 10 NO:1 NO:12

SEQ 10 NO:8

(+ CLOSING)

AAS-12 OF SEQ 10 NO:1

lys Ser Ser lys Cys

REQUEST
JAN

STAFF USE ONLY

Date completed:

9/13/00

Searcher:

Jan

Terminal time:

40

Elapsed time:

CPU time:

+ 10/

Total time:

Number of Searches:

2

Number of Databases:

Search Site

STIC

CM-1

Pre-S

Type of Search

N.A. Sequence

A.A. Sequence

Structure

Bibliographic

Vendors

IG

STN

Dialog

APS

Geninfo

SDC

DARC/Questel

Other

=> fil reg

FILE 'REGISTRY' ENTERED AT 07:04:18 ON 13 SEP 2000
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PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
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STRUCTURE FILE UPDATES: 12 SEP 2000 HIGHEST RN 288839-14-5
DICTIONARY FILE UPDATES: 12 SEP 2000 HIGHEST RN 288839-14-5

TSCA INFORMATION NOW CURRENT THROUGH JANUARY 11, 2000

Please note that search-term pricing does apply when
conducting SmartSELECT searches.

Structure search limits have been increased. See HELP SLIMIT
for details.

=> e ksskc/sqep

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E2	1	KSSKAVAAWTLKAAAVNIRNCCYI/SQEP
E3	0 -->	KSSKC/SQEP
E4	1	KSSKESSKKPKENKPLKEEKIVPKMAFKEPKPMSKEPKPDSNLLTITSGQDKKAPSKRPP ISDSEELSAKKRKKSSSEALFKSFSSAPPLILTCSADKKQIKDKSHVKGKVKIESETSE KKKSTLPPFDDIVDPNDSVEENISSKSDSEQSPASSSSSSSSSFTPSQTRQQGPLRSI MKDLHSDDDNEEESDEVEDND/SQEP
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E8	1	KSSKLVSANRLFG/SQEP
E9	1	KSSKSPSKKKKKKPGDC/SQEP
E10	2	KSSL/SQEP
E11	1	KSSLEDQKIKEKLQPAEIETCMKTITITILEWLEKNQLAGKDEYEAKNKEAESVCAPIMSK IYQD/SQEP
E12	1	KSSLEEPDFYKTKIK/SQEP

=> d his

(FILE 'HOME' ENTERED AT 06:58:21 ON 13 SEP 2000)
SET COST OFF

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E VIDHQGTKSSKCVRQKVEGSS/SQEP

L1 1 S E3

FILE 'HCAOLD' ENTERED AT 06:59:13 ON 13 SEP 2000
0 S L1

FILE 'HCAPLUS' ENTERED AT 06:59:15 ON 13 SEP 2000
L3 1 S L1
SEL RN

FILE 'REGISTRY' ENTERED AT 06:59:40 ON 13 SEP 2000
L4 32 S E1-E32
L5 14 S L4 AND PROTEIN/FS
L6 18 S L4 NOT L5
L7 17 S L6 AND NUCLEIC/FS

Point of Contact:
Jan Delaval
Librarian-Physical Sciences
CM1 1E01 Tel: 308-4498

L8 3 S L7 AND 747/SQL
L9 4 S L7 AND 750/SQL

FILE 'HCAOLD' ENTERED AT 07:01:28 ON 13 SEP 2000
L10 0 S L8 OR L9

FILE 'HCAPLUS' ENTERED AT 07:01:31 ON 13 SEP 2000
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L12 1 S L3,L11
L13 0 S LYS SER SER LYS CYS
L14 1 S KSSKC
L15 1 S L12,L14

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L16 1 S L1 OR L8 OR L9
L17 0 S KSSKC

FILE 'HCAPLUS, USPATFULL' ENTERED AT 07:04:02 ON 13 SEP 2000
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E KSSKC/SQEP

=> d sqide can l1

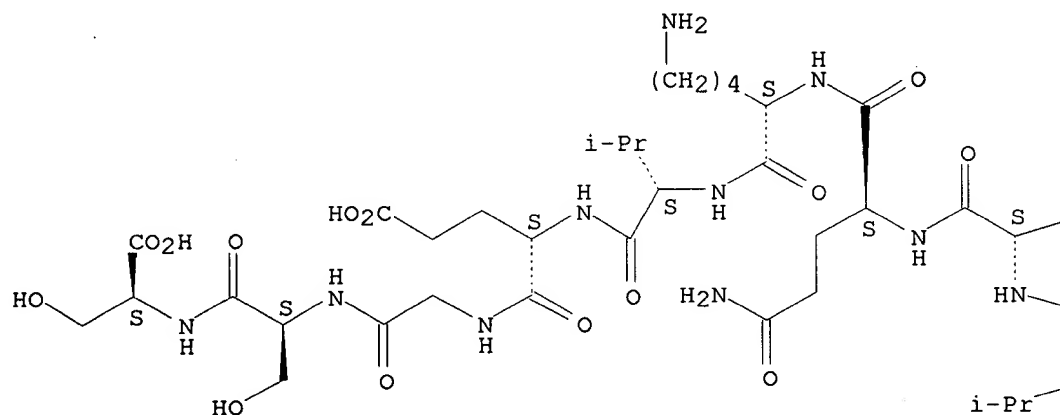
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RN 172998-82-2 REGISTRY
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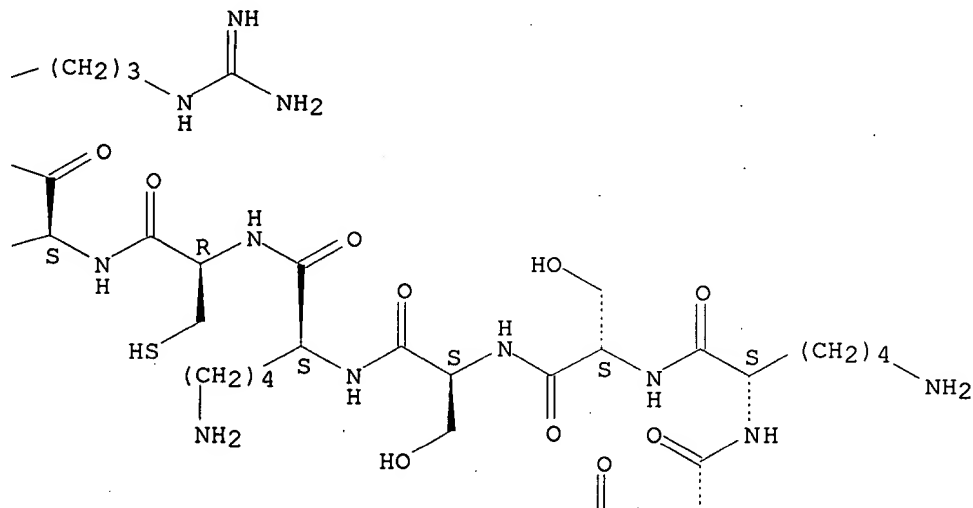
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LC STN Files: CA, CAPLUS, TOXLIT, USPATFULL

Absolute stereochemistry.

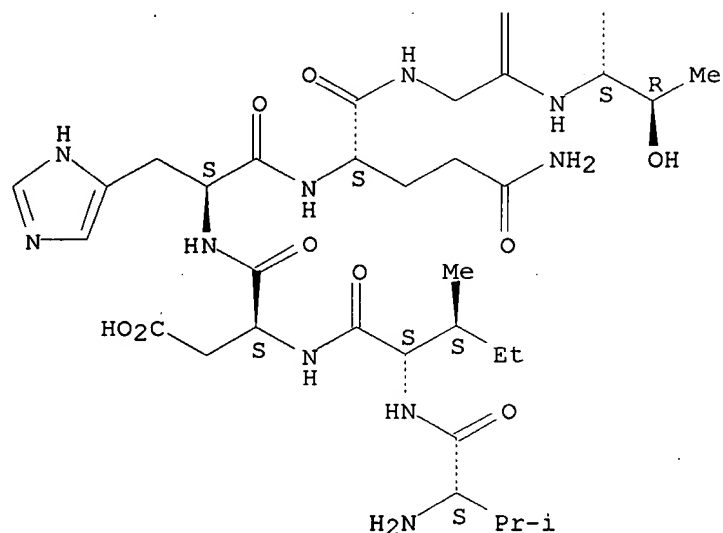
PAGE 1-A



PAGE 1-B



PAGE 2-B



1 REFERENCES IN FILE CA (1967 TO DATE)
 1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 124:127101

=> d sqide can 18 tot

L8 ANSWER 1 OF 3 REGISTRY COPYRIGHT 2000 ACS

RN 173012-28-7 REGISTRY

CN DNA (human-mouse clone 5G1.1 scFv DO12 immunoglobulin G1 anti-antigen CD 5-specifying) (9CI) (CA INDEX NAME)

OTHER CA INDEX NAMES:

CN Deoxyribonucleic acid (human-mouse clone 5G1.1 scFv DO12 immunoglobulin G1 anti-antigen CD 5-specifying)
FS NUCLEIC ACID SEQUENCE
SQL 747
NA 159 a 189 c 211 g 188 t
NTE doublestranded

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       151 tacggtgcga cgaacctggc agatggagtc cttctcgcgt tctctggatc
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       601 tcgactagta cagtatacat ggagctctcc agcctgcgat cggaggacac
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MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXLIT, USPATFULL
1 REFERENCES IN FILE CA (1967 TO DATE)
1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 124:127101

L8 ANSWER 2 OF 3 REGISTRY COPYRIGHT 2000 ACS

RN 173012-11-8 REGISTRY

CN DNA (human-mouse clone 5G1.1 scFv immunoglobulin G1 anti-antigen CD 5-specifying) (9CI) (CA INDEX NAME)

OTHER CA INDEX NAMES:

CN Deoxyribonucleic acid (human-mouse clone 5G1.1 scFv immunoglobulin G1 anti-antigen CD 5-specifying)

FS NUCLEIC ACID SEQUENCE

SQL 747

NA 161 a 186 c 209 g 191 t

NTE doublestranded

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MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXLIT, USPATFULL
1 REFERENCES IN FILE CA (1967 TO DATE)
1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 124:127101

L8 ANSWER 3 OF 3 REGISTRY COPYRIGHT 2000 ACS

RN 173012-09-4 REGISTRY

CN DNA (mouse clone 5G1.1M1 scFv immunoglobulin G1 anti-antigen CD 5-specifying cDNA) (9CI) (CA INDEX NAME)

OTHER CA INDEX NAMES:

CN Deoxyribonucleic acid (mouse clone 5G1.1M1 scFv immunoglobulin G1 anti-antigen CD 5-specifying messenger RNA-complementary)

FS NUCLEIC ACID SEQUENCE

SQL 747

NA 183 a 174 c 211 g 179 t

NTE doublestranded

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     201 tggatctggt agacagtatt atctcaagat cagtagcctg catcctgacg
     251 atgttgcaac gtattactgt caaaatgtgt taaatactcc tctcacgttc
     301 ggtgctggga ccaagttgga gctgaaacgg accggaggtg gcgggtcggg
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MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXLIT, USPATFULL

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 124:127101

=> d sqide can 19 tot

L9 ANSWER 1 OF 4 REGISTRY COPYRIGHT 2000 ACS

RN 173012-26-5 REGISTRY

CN DNA (human-mouse clone 5G1.1VH+IGHRLD immunoglobulin G1 anti-antigen CD 5-specifying) (9CI) (CA INDEX NAME)

OTHER CA INDEX NAMES:

CN Deoxyribonucleic acid (human-mouse clone 5G1.1VH+IGHRLD immunoglobulin G1 anti-antigen CD 5-specifying)

FS NUCLEIC ACID SEQUENCE

SQL 750

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NTE doublestranded

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CI MAN
SR CA
LC STN Files: CA, CAPLUS, TOXLIT, USPATFULL
1 REFERENCES IN FILE CA (1967 TO DATE)
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REFERENCE 1: 124:127101

L9 ANSWER 2 OF 4 REGISTRY COPYRIGHT 2000 ACS
RN 173012-18-5 REGISTRY
CN DNA (human-mouse clone 5G1.1 VH + IGHRLC immunoglobulin G1 anti-antigen CD 5-specifying cDNA) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid (human-mouse clone 5G1.1 VH + IGHRLC immunoglobulin G1 anti-antigen CD 5-specifying messenger RNA-complementary)
FS NUCLEIC ACID SEQUENCE
SQL 750
NA 163 a 220 c 197 g 170 t
NTE doublestranded

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MF Unspecified
CI MAN
SR CA
LC STN Files: CA, CAPLUS, TOXLIT, USPATFULL
1 REFERENCES IN FILE CA (1967 TO DATE)
1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 124:127101

L9 ANSWER 3 OF 4 REGISTRY COPYRIGHT 2000 ACS
RN 173012-16-3 REGISTRY
CN DNA (human-mouse clone 5G1.1VH+IGHRL immunoglobulin G1 anti-antigen CD 5-specifying) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid (human-mouse clone 5G1.1VH+IGHRL immunoglobulin G1 anti-antigen CD 5-specifying)
FS NUCLEIC ACID SEQUENCE
SQL 750
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NTE doublestranded

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MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXLIT, USPATFULL

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 124:127101

L9 ANSWER 4 OF 4 REGISTRY COPYRIGHT 2000 ACS

RN 173012-15-2 REGISTRY

CN DNA (human-mouse clone 5G1.1M1 VH +HuG1 immunoglobulin G1 anti-antigen CD 5-specifying) (9CI) (CA INDEX NAME)

OTHER CA INDEX NAMES:

CN Deoxyribonucleic acid (human-mouse clone 5G1.1M1 VH +HuG1 immunoglobulin G1 anti-antigen CD 5-specifying)

FS NUCLEIC ACID SEQUENCE

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NTE doublestranded

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MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXLIT, USPATFULL

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 124:127101

=> fil hcaplus uspatful

FILE 'HCAPLUS' ENTERED AT 07:04:53 ON 13 SEP 2000

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FILE 'USPATFULL' ENTERED AT 07:04:53 ON 13 SEP 2000

CA INDEXING COPYRIGHT (C) 2000 AMERICAN CHEMICAL SOCIETY (ACS)

=> d bib abs hitrn tot

L18 ANSWER 1 OF 2 HCAPLUS COPYRIGHT 2000 ACS
 AN 1996:73261 HCAPLUS
 DN 124:127101
 TI Anti-complement C5 antibodies for the treatment of glomerulonephritis and other inflammatory diseases
 IN Evans, Mark J.; Matis, Louis; Mueller, Eileen Elliott; Nye, Steven H.; Rollins, Scott; Rother, Russell P.; Springhorn, Jeremy P.; Squinto, Stephen P.; Thomas, Thomas C.; et al.
 PA Alexion Pharmaceuticals, Inc., USA
 SO PCT Int. Appl., 159 pp.
 CODEN: PIXXD2
 DT Patent
 LA English
 FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9529697	A1	19951109	WO 1995-US5688	19950501
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	RW: KE, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
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	AU 9524747	A1	19951129	AU 1995-24747	19950501
	EP 758904	A1	19970226	EP 1995-919041	19950501
	R: AT, BE, CH, DE, DK, ES, FR, GB, IE, IT, LI, NL, PT, SE				
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	JP 10500289	T2	19980113	JP 1995-528523	19950501
PRAI	US 1994-236208		19940502		
	WO 1995-US5688		19950501		
AB	The use of anti-C5 antibodies, e.g., monoclonal antibodies, to treat glomerulonephritis (GN) is disclosed. The administration of such antibodies at low dosage levels has been found to significantly reduce glomerular inflammation/enlargement and other pathol. conditions assocd. with GN. Also disclosed are novel anti-C5 antibodies and anti-C5 antibody-encoding nucleic acid mols. These antibodies are useful in the treatment of GN and other inflammatory conditions involving pathol. activation of the complement system.				
IT	172998-82-2P RL: BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses) (epitope KSSKC -contg. antigen; anti-complement C5 antibodies for the treatment of glomerulonephritis and other inflammatory diseases)				
IT	173012-09-4P 173012-11-8P 173012-15-2P 173012-16-3P 173012-18-5P 173012-26-5P 173012-28-7P RL: BAC (Biological activity or effector, except adverse); BOC (Biological occurrence); BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation); USES (Uses) (nucleic acid sequence; anti-complement C5 antibodies for the treatment of glomerulonephritis and other inflammatory diseases)				

L18 ANSWER 2 OF 2 USPATFULL
 AN 2000:73908 USPATFULL
 TI Use of antibodies specific to human complement component C5 for the treatment of glomerulonephritis
 IN Wang, Yi, Orange, CT, United States
 Matis, Louis, Southport, CT, United States
 Rollins, Scott, Monroe, CT, United States
 PA Alexion Pharmaceuticals, Inc., New Haven, CT, United States (U.S. corporation)

PI US 6074642 20000613
AI US 1994-236208 19940502 (8)
DT Utility
EXNAM Primary Examiner: Feisse, Lila; Assistant Examiner: Gambel, Phillip
LREP Fidel, Seth A.; Klee, Maurice M.
CLMN Number of Claims: 5
ECL Exemplary Claim: 1
DRWN 14 Drawing Figure(s); 7 Drawing Page(s)
LN.CNT 1197

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The use of anti-C5 antibodies, e.g., monoclonal antibodies, to treat glomerulonephritis (GN) is disclosed. The administration of such antibodies at low dosage levels has been found to significantly reduce glomerular inflammation/enlargement and other pathologic conditions associated with GN.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

IT **172998-82-2P**
(epitope KSSKC-contg. antigen; anti-complement C5 antibodies for the treatment of glomerulonephritis and other inflammatory diseases)
IT **173012-09-4P 173012-11-8P 173012-15-2P**
173012-16-3P 173012-18-5P 173012-26-5P
173012-28-7P
(nucleic acid sequence; anti-complement C5 antibodies for the treatment of glomerulonephritis and other inflammatory diseases)

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MSPrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Sep 6 08:22:05 2000; Maspar time 4.08 Seconds

Tabular output not generated. 57.866 Million cell updates/sec

Title: >US-08-487-283A-1
Description: (8-12) from US08487283A.pep
Perfect Score: 35
Sequence: 1 KSKC 5

Scoring table:
PAM 150
Gap 15

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0%
Listing first 1000 summaries
Maximum DB seq length 5

Database: pIr64
1:PIr1 2:PIr2 3:PIr3 4:PIr4

Statistics: Mean 16.465; Variance 17.344; scale 0.949

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	ID	Description	Pred. No.

No matches found.

Search completed: Wed Sep 6 08:23:04 2000
Job time : 59 secs.

M P E R C H
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Mserch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Sep 6 08:19:32 2000; MasPar time 2.56 Seconds

Tabular output not generated. 60.533 Million cell updates/sec

Title: >US-08-487-283A-1
Description: (8-12) from US08487283A.pep
Perfect Score: 35
Sequence: 1 KSKC 5

Scoring table: PAM 150
Gap 15

Searched: 85661 seqs, 30989116 residues

Post-processing: Minimum Match 0%
Listing first 1000 summaries
Maximum DB seq length 5

Database: swiss-prot38
1:swissprot

Statistics: Mean 16.989; Variance 16.059; scale 1.058

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	ID	Description	Pred. No.

No matches found.

Search completed: Wed Sep 6 08:20:17 2000
Job time : 45 secs.

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Msrch_PP protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Sep 6 08:20:34 2000; MasPar time 5.75 Seconds

Tabular output not generated. 60.308 Million cell updates/sec

Title: >US-08-487-283A-1
Description: (8-12) from US08487283A.pep
Perfect Score: 35
Sequence: 1 KSSKC 5

Scoring table: PAM 150
Gap 15

Searched: 225878 segs, 69334122 residues

Post-processing: Minimum Match 0%
Listing first 1000 summaries
Maximum DB seq length 5

Database: sptrembl12
1:sp_archaea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_protein 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 16.549; Variance 15.598; scale 1.061

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match length	ID	Description	Pred. No.

No matches found.

Search completed: Wed Sep 6 08:21:48 2000
Job time : 74 secs.

MIPERCH
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MIPerch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Sep 6 08:23:22 2000; MasPar time 2.62 Seconds

Tabular output not generated. 45.269 Million cell updates/sec

Title: >US-08-487-283A-1
Description: (8-12) from US08487283A.pep
Perfect Score: 35
Sequence: 1 KSKC 5

Scoring table: PAM 150
Gap 15

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%
Listing first 1000 summaries
Maximum DB seq length 5

Database: a-geneseq36
1:geneseqp

Statistics: Mean 12.105; Variance 34.177; scale 0.354

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					
No.	Score	Match	Length	ID	Description	Pred. No.

No matches found.

Search completed: Wed Sep 6 08:24:11 2000
Job time : 49 secs.

MIPSOL
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Msrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Sep 6 08:25:39 2000; MasPar time 12.13 Seconds

Tabular output not generated. 50.906 Million cell updates/sec

Title: >US-08-487-283A-1

Description: (8-12) from US08487283A.pep

Perfect Score: 35

Sequence: 1 KSKC 5

Scoring table: PAM 150

Gap 15

Searched: 820620 seqs, 123522873 residues

Post-processing: Minimum Match 0%

Listing first 1000 summaries

Maximum DB seq length 5

Database: a-pending

1:PCF 2:U6 3:U60 4:U7 5:U80 6:U81 7:U82 8:U83 9:U84A

10:U84B 11:U85 12:U86 13:U87 14:U88 15:U89 16:U90 17:U91

18:U92 19:U93 20:U94 21:U95 22:NEWP 23:NEWU60 24:NEWU7

25:NEWU8 26:NEWU9

Statistics: Mean 13.804; Variance 29.044; scale 0.475

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					
No.	Score	Match	Length	DB	ID	Description
						Pred. No.

No matches found.

Search completed: Wed Sep 6 08:27:12 2000

Job time : 93 secs.

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Mperch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Sep 6 08:24:29 2000; Maspar time 2.21 Seconds

Tabular output not generated. 34.699 Million cell updates/sec

Title: >US-08-487-283A-1

Description: (8-12) from US08487283A.pep

Perfect Score: 35

Sequence: 1 KSSKC 5

Scoring table: PAM 150
Gap 15

Searched: 152433 seqs, 15329240 residues

Post-processing: Minimum Match 0%

Listing first 1000 summaries

Maximum DB seq length 5

Database: a-issued

1:5A_COMB 2:5B_COMB 3:6_COMB 4:PCT_COMB 5:backfiles1

Statistics: Mean 11.504; Variance 33.907; scale 0.339

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	ID	Description	Pred. No.

No matches found.							

Search completed: Wed Sep 6 08:25:20 2000
Job time : 51 secs.

MUSE (TM)

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Msrch:lp protein - protein database search, using Smith-Waterman algorithm
Run on: Wed Sep 6 08:16:42 2000; MasPar time 4.45 seconds
Tabular output not generated. 222.630 Million cell updates/sec

Title: >US-08-487-283A-1
Description: (1-21) from US08487283A.pep
Perfect Score: 141
Sequence: 1 VIDHOGTKSSKCVRKVEGSS 21

Scoring table: PAM 150
Gap 15

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir64
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 25.757; Variance 31.889; scale 0.808

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	141	100.0	1676	1 C5HU	complement C5 precursor	2.35e-22
2	69	48.9	1680	1 C5MS	complement C5 precursor	3.83e-03
3	68	48.2	936	2 H71862	probable cytochrome C	6.49e-03
4	65	46.1	936	2 B64567	cytochrome c biogenesis	3.07e-02
5	63	44.7	213	2 T10422	MADS box protein A -	8.46e-02
6	62	44.0	213	2 S76070	hypothetical protein	1.39e-01
7	61	43.3	214	2 T00879	MADS box protein AG2	2.29e-01
8	60	42.6	1166	2 H71609	hypothetical protein	3.74e-01
9	59	41.8	940	2 S45087	lactoferrin binding p	6.08e-01
10	59	41.8	1002	2 A56678	yeamanulein-alpha - f	9.82e-01
11	58	41.1	164	2 A65068	hypothetical protein	9.82e-01
12	58	41.1	205	2 T49364	protein tyrosine phos	9.82e-01
13	58	41.1	223	2 T49365	protein tyrosine phos	9.82e-01
14	58	41.1	259	2 F70677	hypothetical protein	9.82e-01
15	57	40.4	117	2 T68524	ribosomal protein L34	1.58e+00
16	57	40.4	264	2 S28969	N-carbamoylsarcosine	1.58e+00
17	56	39.7	236	2 T01662	globulin-1 - maize (f	2.52e+00
18	56	39.7	407	2 T02258	globulin-1 - maize	2.52e+00
19	56	39.7	537	2 B33485	spore coat protein SP	2.52e+00
20	56	39.7	540	2 S21825	vicillin-like storage	2.52e+00
21	55	39.0	573	2 A53234	globulin-1S, GIBIS -	4.01e+00
22	55	39.0	504	2 H69333	medium-chain acyl-CoA	4.01e+00
23	55	39.0	775	2 A32494	transposable element	4.01e+00

24	55	39.0	1349	2 T13031	nucleoporin - fruit f	4.01e+00
25	55	39.0	1365	2 T13991	nucleoporin 154 - fru	4.01e+00
26	54	38.3	148	2 E47119	spore coat protein (1	6.34e+00
27	54	38.3	224	1 G64383	riboflavin-specific d	6.34e+00
28	54	38.3	249	2 T04307	M79 protein - rice	6.34e+00
29	54	38.3	249	2 T04335	MADS box protein - ri	6.34e+00
30	54	38.3	259	2 T04169	MADS box protein - ri	6.34e+00
31	54	38.3	562	2 S46281	p element - fruit fly	6.34e+00
32	54	38.3	818	1 A30107	dipeptidyl aminopept	6.34e+00
33	54	38.3	889	2 T11742	egg sperm receptor -	6.34e+00
34	54	38.3	1030	2 S57380	probable membrane pro	6.34e+00
35	53	37.6	116	1 Q4ADE2	early E4 11k protein	9.96e+00
36	53	37.6	116	1 Q4ADE5	early E4 11k protein	9.96e+00
37	53	37.6	148	2 S41772	glycine-rich RNA-bind	9.96e+00
38	53	37.6	231	2 T14801	MADS box protein MADS	9.96e+00
39	53	37.6	589	2 C38128	epithelin/granulin pr	9.96e+00
40	53	37.6	591	2 S43428	omega-crystallin - g1	9.96e+00
41	53	37.6	669	2 I54205	galactosylceramidase	9.96e+00
42	53	37.6	918	2 D71407	hypothetical protein	9.96e+00
43	53	37.6	1089	1 PFHUGA	platelet-derived grow	9.96e+00
44	53	37.6	1144	2 A54810	TMV resistance protel	9.96e+00
45	53	37.6	2471	2 A49128	cell-fate determining	9.96e+00

ALIGNMENTS

RESULT	ENTRY	1	ALIGNMENTS
TITLE	C5HU	#type complete	
CONTAINS	complement C5 precursor - human		
ORGANISM	C5a anaphylatoxin; C5b		
DATE	#formal_name Homo sapiens #common_name man		
	30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change		
	18-Jun-1999		
ACCESSIONS	A40075; A27689; A01267; A01266; S15121		
REFERENCE	A40075		
#authors	Haviland, D.L.; Haviland, J.C.; Fleischner, D.T.; Hunt, A.;		
#journal	J. Immunol. (1991) 146:362-368		
#title	Complete cDNA sequence of human complement pro-C5. Evidence		
	of truncated transcripts derived from a single copy gene.		
#cross-references	MUID:91079575		
#accession	A40075		
#molecule_type	mRNA		
#residues	1-1676 #label HAV		
#cross-references	GB:M57729; NID:g179982; PIDN:AAA51925.1; PID:g179983		
#note	518-Ser was also found		
REFERENCE	A27689		
#authors	Wetzel, R.A.; Lemons, R.S.; Le Beau, M.M.; Barnum, S.R.;		
#journal	Biochemistry (1988) 27:1474-1482		
#title	Molecular analysis of human complement component C5:		
	localization of the structural gene to chromosome 9.		
#cross-references	MUID:88209511		
#accession	A27689		
#molecule_type	mRNA		
#residues	412-1676 #label WET		
#cross-references	GB:M65134; GB:M18679; NID:g179691; PIDN:AAA51856.1;		
	PID:g179692		
REFERENCE	A01267		
#authors	Fernandez, H.N.; Hugli, T.E.		
#journal	J. Biol. Chem. (1978) 253:6955-6964		
#title	Primary structural analysis of the polypeptide portion of		
	human C5a anaphylatoxin. Polypeptide sequence determination		
	and assignment of the oligosaccharide attachment site in		
	C5a.		
#cross-references	MUID:79005687		
#accession	A01267		
#molecule_type	protein		
#residues	678-751 #label FER		
REFERENCE	A01266		
#authors	Lundwall, A.B.; Wetzel, R.A.; Kristensen, T.; Whitehead,		
	A.S.; Woods, D.E.; Ogden, R.C.; Colten, H.R.; Tack, B.F.		
#journal	J. Biol. Chem. (1985) 260:2108-2112		


```

:::|:|:|:|:|:|
OY      4  HOGTKSSKCVROKVE 18

RESULT  12
ENTRY   I49364      #type complete
TITLE   protein tyrosine phosphatase - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE     02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
17-Mar-1999

ACCESSIONS
REFERENCE
#authors Wisnart, M.J.; Denu, J.M.; Williams, J.A.; Dixon, J.E.
#journal J. Biol. Chem. (1995) 270:26782-26785
#title A single mutation converts a novel-phosphotyrosine binding
domain into a dual-specificity phosphatase.
#cross-references MUID:96070766
#accession I49364
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-205 #label RES
#cross-references EMBL:U34973; NID:q1063624; PID:q1063625

CLASSIFICATION
#superfamily VHL-type dual specificity phosphoprotein
phosphatase homology

FEATURE
36-174
#domain VHL-type dual specificity phosphoprotein
phosphatase homology #label VHL
#length 223 #molecular_weight 25416 #checksum 359

SUMMARY
Query Match 41.1%; Score 58; DB 2; Length 223;
Best Local Similarity 25.0%; Pred. No. 9.82e-01;
Matches 5; Conservative 9; Mismatches 6; Indels 0; Gaps 0.

Db 51 ILKRGITHICIRONIEAN 70
:::|:|:|:|:|:|
OY      1  VIDHGTSSKCVROKVEG 20

RESULT  13
ENTRY   I49365      #type complete
TITLE   protein tyrosine phosphatase - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE     02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
17-Mar-1999

ACCESSIONS
REFERENCE
#authors Wisnart, M.J.; Denu, J.M.; Williams, J.A.; Dixon, J.E.
#journal J. Biol. Chem. (1995) 270:26782-26785
#title A single mutation converts a novel-phosphotyrosine binding
domain into a dual-specificity phosphatase.
#cross-references MUID:96070766
#accession I49365
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-223 #label RES
#cross-references EMBL:U34973; NID:q1063624; PID:q1063626

CLASSIFICATION
#superfamily VHL-type dual specificity phosphoprotein
phosphatase homology

FEATURE
36-174
#domain VHL-type dual specificity phosphoprotein
phosphatase homology #label VHL
#length 223 #molecular_weight 25416 #checksum 359

SUMMARY
Query Match 41.1%; Score 58; DB 2; Length 223;
Best Local Similarity 25.0%; Pred. No. 9.82e-01;
Matches 5; Conservative 9; Mismatches 6; Indels 0; Gaps 0.

Db 51 ILKRGITHICIRONIEAN 70
:::|:|:|:|:|:|
OY      1  VIDHGTSSKCVROKVEG 20

```

```
RESULT 14
ENTRY
TITLE      F70677      #type complete
            hypothetical protein RV3549c - Mycobacterium tuberculosis
            (strain H37Rv)
ORGANISM    #formal_name Mycobacterium tuberculosis
DATE        17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
            26-Aug-1999
ACCESSIONS  F70677
REFERENCE   AF0500
#authors    Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher,
            C.; Harris, D.; Gordon, S.V.; Eiglmeier, K.; Gas, S.; Barry
            III, C.E.; Tekala, F.; Badcock, K.; Basham, D.; Brown, D.;
            Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.;
            Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
            Hornsby, T.; Jagels, K.; Krogh, A.; McLean, J.; Moule, S.;
            Murphy, L.; Oliver, S.; Osborne, J.; Quail, M.A.;
            Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.;
            Skelton, S.; Squares, S.; Squires, R.; Sulston, J.E.;
            Taylor, K.; Whitehead, S.; Barrell, B.G.
#journal    Nature (1998) 393:537-544
#title      Deciphering the biology of Mycobacterium tuberculosis from
            the complete genome sequence.
#cross-references MUID:98295987
#accession  F70677
#status     preliminary; nucleic acid sequence not shown;
            translation not shown
#molecule_type DNA
#residues   1-259 #label COL
#cross-references GB:282098; GB:AL123456; NID:g3261664; PID:e280727;
            PID:gl66611
#experimental_source strain H37Rv
GENETICS
#gene       RV3549c
CLASSIFICATION #superfamily ribitol dehydrogenase; short-chain alcohol
            dehydrogenase homology
FEATURE
17-185      #domain short-chain alcohol dehydrogenase homology
            #label SADH
SUMMARY      #length 259 #molecular-weight 26855 #checksum 5885
Query Match 41.1%; Score 58; DB 2; Length 259;
Best Local Similarity 36.8%; Pred. No. 9.82e-01;
Matches      7; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
Db          35 VFAEQGATVITCARRVDG 53
            | : ||: | : | : |
QY          1 VIDHQGTRKSKCVQRKVEG 19

RESULT 15
ENTRY
TITLE      I68524      #type complete
            ribosomal protein L34 - human
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        24-May-1996 #sequence_revision 24-May-1996 #text_change
            13-Aug-1999
ACCESSIONS  I68524
REFERENCE   I54209
#authors    Rommens, J.M.; Durocher, F.; McArthur, J.; Tonin, P.;
            Leblanc, J.
#journal    Genomics (1995) 28:530-542
#title      Generation of a transcription map at the HSD17B locus
            centromeric to BRCA1 at 17q21.
#cross-references MUID:96039267
#accession  I68524
#status     preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues   1-117 #label RES
#cross-references GB:L38941; NID:gl008855; PIDN:AAC41916.1;
            PID:gl008856
CLASSIFICATION #superfamily rat ribosomal protein L34
SUMMARY      #length 117 #molecular-weight 13305 #checksum 4392
```

```
Query Match 40.4%; Score 57; DB 2; Length 117;
Best Local Similarity 41.7%; Pred. No. 1.58e+00;
Matches      5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
Db          80 GSMCAKCVRDRI 91
            | : ||| : |
QY          6 GTKSKSKCVQRKV 17
```

Search completed: Wed Sep 6 08:17:01 2000
Job time : 19 secs.

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MPsrch.pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Sep 6 08:15:20 2000; MasPar time 2.98 Seconds

Tabular output not generated. 218.703 Million cell updates/sec

Title: >US-08-487-283A-1
 Description: (1-21) from US08487283A.pep
 Perfect Score: 141
 Sequence: 1 VIDHGTSSKCVKVEGSS 21

Scoring table: PAM 150
 Gap 15

Searched: 85661 seqs, 30989116 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: swiss-prot38
 1:swissprot

Statistics: Mean 26.489; Variance 29.186; scale 0.908

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	141	100.0	1676	1	CO5_HUMAN	COMPLEMENT C5 PRECURSOR	3.33e-25
2	69	48.9	1680	1	CO5_MOUSE	COMPLEMENT C5 PRECURSOR	7.23e-04
3	60	42.6	425	1	IM44_CAEEL	PROBABLE MITOCHONDRIAL	1.11e-01
4	59	41.8	943	1	IROA_NEIME	IRON-REGULATED OUTER M	1.88e-01
5	59	41.8	1002	1	YEMA_DROME	YEMANUCLEIN-ALPHA	1.88e-01
6	58	41.1	160	1	YOEJ_ECOLI	HYPOTHETICAL 18.7 KDA	3.19e-01
7	57	40.4	116	1	RL34_HUMAN	60S RIBOSOMAL PROTEIN	5.36e-01
8	57	40.4	264	1	CSH_ARTSP	N-CARBAOXYLARSOCINE A	5.36e-01
9	56	39.7	89	1	IT16_ARATH	PUTATIVE TRYPSIN INHIB	8.95e-01
10	56	39.7	537	1	SP70_DICDI	SPORE COAT PROTEIN SP7	8.95e-01
11	56	39.7	573	1	GLB1_MAIZE	GLOBULIN-1 S ALLELE PR	8.95e-01
12	56	39.7	1357	1	RPOB_PSEPU	DNA-DIRECTED RNA POLIM	8.95e-01
13	55	39.0	775	1	YTX1_XENLA	TRANSPOSON TX1 HYPOTHE	2.44e+00
14	54	38.3	148	1	CORT2_BACSU	SPORE COAT PROTEIN 2	2.44e+00
15	54	38.3	224	1	RIB7_METJA	PUTATIVE 5'-AMINO-6-(5-	2.44e+00
16	54	38.3	818	1	DAR2_YEAST	DIPEPTIDYL AMINOPEPTID	2.44e+00
17	54	38.3	889	1	HS97_STRPU	97 KDA HEAT SHOCK PROT	2.44e+00
18	54	38.3	1039	1	YR11_CAEEL	HYPOTHETICAL 118.2 KDA	2.44e+00
19	53	37.6	116	1	E411_ADE02	PROBABLE EARLY E4 11 K	4.00e+00
20	53	37.6	116	1	E411_ADE05	PROBABLE EARLY E4 11 K	4.00e+00
21	53	37.6	589	1	GRN_MOUSE	GRANULINS PRECURSOR (A	4.00e+00
22	53	37.6	669	1	GAIC_HUMAN	GALACTOCEPHEROSIDASE P	4.00e+00
23	53	37.6	669	1	GAIC_MOUSE	GALACTOCEPHEROSIDASE P	4.00e+00

24	53	37.6	1089	1	PGDS_HUMAN	ALPHA PLATELET-DERIVED	4.00e+00
25	52	36.9	64	1	BFD_SERMA	BACTERIOFERITIN-ASSOC	6.49e+00
26	52	36.5	121	1	RK14_GUTTH	CHLOROPLAST 50S RIBOS	6.49e+00
27	52	36.9	185	1	EPF_BACFR	ELONGATION FACTOR P (E	6.49e+00
28	52	36.5	329	1	ESG2_TRYB	VEG EXPRESSION SITE-AS	6.49e+00
29	52	36.5	354	1	OCG_AGR75	ORNITHINE CYCLODEAMINA	6.49e+00
30	52	36.9	455	1	P2X5_RAT	P2X PURINORECEPTOR 5	6.49e+00
31	52	36.9	1620	1	MTDM_MOUSE	DNA (CYTOSINE-5)-METHY	6.49e+00
32	51	36.2	121	1	R34A_YEAST	60S RIBOSOMAL PROTEIN	1.04e+01
33	51	36.2	121	1	R34B_YEAST	60S RIBOSOMAL PROTEIN	1.04e+01
34	51	36.2	337	1	ADH1_ZYMO	ALCOHOL DEHYDROGENASE	1.04e+01
35	51	36.2	337	1	VP67_NPVGM	MAJOR ENVELOPE GLYCOP	1.04e+01
36	51	36.2	470	1	KPY1_ECOLI	PYRUVATE KINASE I (EC	1.04e+01
37	51	36.2	470	1	KPY1_SALTY	PYRUVATE KINASE I (EC	1.04e+01
38	51	36.2	512	1	VP67_NPVAC	MAJOR ENVELOPE GLYCOP	1.04e+01
39	51	36.2	574	1	ESR1_ONCMY	ESTROGEN RECEPTOR (ER)	1.04e+01
40	51	36.2	588	1	GRN_RAT	GRANULINS PRECURSOR (A	1.04e+01
41	51	36.2	1056	1	MUC5_HUMAN	TRACHEOBRONCHIAL MUCIN	1.04e+01
42	51	36.2	1129	1	JAK2_MOUSE	TYROSINE-PROTEIN KINAS	1.04e+01
43	51	36.2	1132	1	JAK2_RAT	TYROSINE-PROTEIN KINAS	1.04e+01
44	51	36.2	1651	1	VIT6_CAEEL	VITELLOGENIN 6 PRECURS	1.04e+01
45	51	36.2	1678	1	CLH_DROME	CLAIRHIN HEAVY CHAIN.	1.04e+01

ALIGNMENTS

RESULT	ID	STANDARD	PRT	1676 AA.
1	ID	CO5_HUMAN		
AC	P01031	21-JUL-1986 (Rel. 01, Created)		
DT	01-DEC-1992 (Rel. 35, last sequence update)			
DT	01-NOV-1997 (Rel. 24, last annotation update)			
DE	COMPLEMENT C5 PRECURSOR [CONTAINS: C5A ANAPHYLATOXIN].			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
NC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
LN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 91079575.			
RA	Haviland D.L., Haviland J.C., Fleischner D.T., Hunt A., Wetsel R.A.;			
RT	"Complete cDNA sequence of human complement pro-C5. Evidence of			
RL	truncated transcripts derived from a single copy gene.";			
RL	J. Immunol. 146:362-368(1991).			
RN	[2]			
RP	SEQUENCE OF 412-1676 FROM N.A.			
RX	MEDLINE: 88209511.			
RA	Wetsel R.A., Lemons R.S., Lebeau M.M., Barnum S.R., Noack D.,			
RT	Tack B.F.;			
RL	"Molecular analysis of human complement component C5: localization of			
RL	the structural gene to chromosome 9.";			
RL	Biochemistry 27:1474-1482(1988).			
RN	[3]			
RP	SEQUENCE OF 412-902 FROM N.A.			
RX	MEDLINE: 85130937.			
RA	Lundvall A.B., Wetsel R.A., Kristensen T., Whitehead A.S.,			
RT	Woods D.E., Ogden R.C., Colten H.R., Tack B.F.;			
RL	"Isolation and sequence analysis of a cDNA clone encoding the fifth			
RL	complement component.";			
RL	J. Biol. Chem. 260:2108-2112(1985).			
RN	[4]			
RP	SEQUENCE OF 678-751.			
RX	MEDLINE: 79005687.			
RA	Fernandez H.N., Hugel T.E.;			
RT	"Primary structural analysis of the polypeptide portion of human C5a			
RT	anaphylatoxin. Polypeptide sequence determination and assignment of			
RT	the oligosaccharide attachment site in C5a.";			
RL	J. Biol. Chem. 253:6955-6964(1978).			
RN	[5]			
RP	SEQUENCE OF 678-751 FROM N.A.			
RX	MEDLINE: 91144547.			
RA	Bohsack J.F., Mollison K.W., Buko A.M., Ashworth J.C., Hall H.R.;			
RT	"Group B streptococci inactivate complement component C5a by enzymic			

RT cleavage at the C-terminus.";
 RL Biochem. J. 273:635-640(1991).
 RN [6]
 RX STRUCTURE BY NMR OF C5A.
 RP MEDLINE; 88309754.
 RA Zuiderweg E.R., Mollison K.W., Henkin J., Carter G.W.;
 RT "Sequence-specific assignments in the 1H NMR spectrum of the human
 RL inflammatory protein C5a";
 RL Biochemistry 27:3568-3580(1988).
 RN [7]
 RP STRUCTURE BY NMR OF C5A.
 RX MEDLINE; 89207527.
 RA Zuiderweg E.R., Nettekheim D.G., Mollison K.W., Carter G.W.;
 RT "Tertiary structure of human complement component C5a in solution
 RL from nuclear magnetic resonance data.";
 RL Biochemistry 28:172-185(1989).
 RN [8]
 RP STRUCTURE BY NMR OF C5A.
 RX MEDLINE; 89274164.
 RA Zuiderweg E.R., Fesik S.W.;
 RT "Heteronuclear three-dimensional NMR spectroscopy of the inflammatory
 RL protein C5a";
 RL Biochemistry 28:2387-2391(1989).
 RN [9]
 RP STRUCTURE BY NMR OF C5A.
 RX MEDLINE; 97160477.
 RA Zhang X., Boyar W., Galakatos N., Gonnella N.C.;
 RT "Solution structure of a unique C5a semi-synthetic antagonist:
 RL implications in receptor binding.";
 RL Protein Sci. 6:65-72(1997).
 RN [10]
 RP STRUCTURE BY NMR OF C5A.
 RX MEDLINE; 97332508.
 RA Zhang X., Boyar W., Toth M.J., Wennogle L., Gonnella N.C.;
 RT "Structural definition of the C5a C terminus by two-dimensional
 RL nuclear magnetic resonance spectroscopy.";
 RL Proteins 28:261-267(1997).
 CC -1- FUNCTION: ACTIVATION OF C5 BY A C5 CONVERTASE INITIATES THE
 CC SPONTANEOUS ASSEMBLY OF THE LATE COMPLEMENT COMPONENTS, C5-C9,
 CC INTO THE MEMBRANE ATTACK COMPLEX. C5B HAS A TRANSIENT BINDING SITE
 CC FOR C6. THE C5B-C6 COMPLEX IS THE FOUNDATION UPON WHICH THE LYCIC
 CC COMPLEX IS ASSEMBLED.
 CC -1- FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C5,
 CC C5 ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT
 CC INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR
 CC PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND
 CC BASOPHILIC LEUKOCYTES. C5A ALSO STIMULATES THE LOCOMOTION OF
 CC POLYMORPHONUCLEAR LEUKOCYTES (CHEMOKINESIS) AND DIRECT THEIR
 CC MIGRATION TOWARD SITES OF INFLAMMATION (CHEMOTAXIS).
 CC -1- SUBUNIT: C5 PRECURSOR IS FIRST PROCESSED BY THE REMOVAL OF 4 BASIC
 CC RESIDUES, FORMING TWO CHAINS, BETA & ALPHA, LINKED BY A DISULFIDE
 CC BOND. C5 CONVERTASE ACTIVATES C5 BY CLEAVING THE ALPHA CHAIN,
 CC RELEASING C5A ANAPHYLATOXIN & GENERATING C5B (BETA CHAIN + ALPHA
 CC CHAIN).
 CC -1- SIMILARITY: TO C3, C4 AND ALPHA-2-MACROGLOBULIN.
 CC -1- SIMILARITY: CONTAINS 1 ANAPHYLATOXIN-LIKE DOMAIN.
 CC -1- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 855
 CC ONWARD DUE TO THE PRESENCE OF AN ALU REPEAT.
 CC -----
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 CC -----
 DR ENBL; M57729; AAA51925.1; -
 DR ENBL; M65134; AAA51856.1; -
 DR PIR; A40075; C5HU.
 DR PIR; S15121; S15121.
 DR PDB; 1KJS; 15-MAY-97.
 DR PDB; 1CFA; 17-SEP-97.

DR MIM; 120900; -
 DR PFAM; PF00207; A2M; 1.
 DR PFAM; PF01835; A2M.N; 1.
 DR PFAM; PF01821; ANATO; 1.
 DR PFAM; PF01759; NTR; 1.
 DR PRINTS; PRO0004; ANAPHYLATOXN.
 DR PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; FALSE_NEG.
 DR PROSITE; PS01177; ANAPHYLATOXIN.1; 1.
 DR PROSITE; PS01178; ANAPHYLATOXIN.2; 1.
 KW Complement pathway; Complement alternate pathway; Glycoprotein;
 KW Plasma; Membrane attack complex; Cytolysis; Inflammatory response;
 KW Signal; Polymorphism; 3D-structure.
 FT SIGNAL 1 18
 FT CHAIN 19 673
 FT PROPEP 674 677
 FT CHAIN 678 1676
 FT PEPTIDE 678 751
 FT CHAIN 752 1676
 FT DOMAIN 698 732
 FT DISULFID 698 724
 FT DISULFID 699 731
 FT DISULFID 711 722
 FT CARBOHYD 741 741
 FT CARBOHYD 911 911
 FT CARBOHYD 1115 1115
 FT CARBOHYD 1630 1630
 FT VARIANT 518 518
 FT /FTID=VAR_001996.
 SQ SEQUENCE 1676 AA; 188331 MW; 87DCAA63FF977D19 CRC64;
 Query Match 100.0%; Score 141; DB 1; Length 1676;
 Best Local Similarity 100.0%; Pred. No. 3.33e-25;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 872 VIDHQGTGSKCVQRKVEGSS 892
 QY 1 VIDHQGTGSKCVQRKVEGSS 21
 RESULT 2
 ID COS_MOUSE STANDARD; PRT; 1680 AA.
 AC P06684;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE COMPLEMENT C5 PRECURSOR [CONTAINS: C5A ANAPHYLATOXIN].
 GN C5 OR HC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wetzel R.A., Fleischer D.T., Haviland D.L.;
 RT "Deficiency of the murine fifth complement component (C5). A 2-base
 RL pair gene deletion in a 5'-exon.";
 RL J. Biol. Chem. 265:2435-2440(1990).
 RN [2]
 RP SEQUENCE OF 41-1680 FROM N.A.
 RX MEDLINE; 87185363.
 RA Wetzel R.A., Ogata R.T., Tack B.F.;
 RT "Primary structure of the fifth component of murine complement.";
 RL Biochemistry 26:737-743(1987).
 CC -1- FUNCTION: ACTIVATION OF C5 BY A C5 CONVERTASE INITIATES THE
 CC SPONTANEOUS ASSEMBLY OF THE LATE COMPLEMENT COMPONENTS, C5-C9,
 CC INTO THE MEMBRANE ATTACK COMPLEX. C5B HAS A TRANSIENT BINDING SITE
 CC FOR C6. THE C5B-C6 COMPLEX IS THE FOUNDATION UPON WHICH THE LYCIC
 CC COMPLEX IS ASSEMBLED.
 CC -1- FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C5,
 CC C5 ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT
 CC INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR
 CC PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND
 CC BASOPHILIC LEUKOCYTES. C5A ALSO STIMULATES THE LOCOMOTION OF

CC POLYMERONUCLEAR LEUKOCYTES (CHEMOKINESIS) AND DIRECT THEIR
 CC MIGRATION TOWARD SITES OF INFLAMMATION (CHEMOTAXIS).
 CC SUBUNIT: C5 PRECURSOR IS FIRST PROCESSED BY THE REMOVAL OF 4 BASIC
 CC RESIDUES, FORMING TWO CHAINS, BETA & ALPHA, LINKED BY A DISULFIDE
 CC BOND. C5 CONVERTASE ACTIVATES C5 BY CLEAVING THE ALPHA CHAIN,
 CC RELEASING C5A ANAPHYLATOXIN & GENERATING C5B (BETA CHAIN + ALPHA
 CC CHAIN).
 CC -1- SIMILARITY: TO C3, C4 AND ALPHA-2-MACROGLOBULIN.
 CC -1- SIMILARITY: CONTAINS 1 ANAPHYLATOXIN-LIKE DOMAIN.
 CC -----
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 CC -----
 CC EMBL: M35525; AAA37349.1; -
 CC EMBL: M35526; AAA37348.1; -
 CC PIR: A27538; A27538.
 CC PIR: A35530; A35530.
 CC HSSP: P01031; 1KJ5.
 CC MGD; MG1:96031; HC.
 CC PFAM: PF00207; A2M; 1.
 CC PFAM: PF01835; A2M_N; 1.
 CC PFAM: PF01821; ANATO; 1.
 CC PFAM: PF01759; NTR; 1.
 CC PRINTS; PRO0004; ANAPHYLATOXN.
 CC PROSITE; PS00477; ALPHA_2-MACROGLOBULIN; FALSE_NEG.
 CC PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
 CC PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
 CC KW Complement pathway: Complement alternate pathway: Glycoprotein;
 CC plasma: Membrane attack complex; Cytolysis; Inflammatory response;
 CC Signal.
 CC FT SIGNAL 1 18
 CC FT CHAIN 19 1680 COMPLEMENT C5.
 CC FT CHAIN 19 674 COMPLEMENT C5 BETA CHAIN.
 CC FT PROPEP 675 678
 CC FT CHAIN 679 1680 COMPLEMENT C5 ALPHA CHAIN.
 CC FT PEPTIDE 679 755 C5A ANAPHYLATOXIN.
 CC FT CHAIN 756 1680 C5B (ALPHA').
 CC FT DOMAIN 702 736 ANAPHYLATOXIN-LIKE.
 CC FT DISULFID 702 728 BY SIMILARITY.
 CC FT DISULFID 703 735 BY SIMILARITY.
 CC FT DISULFID 715 736 BY SIMILARITY.
 CC FT CARBOHYD 427 427 POTENTIAL.
 CC FT CARBOHYD 915 915 POTENTIAL.
 CC FT CARBOHYD 1119 1119 POTENTIAL.
 CC FT CARBOHYD 1633 1633 POTENTIAL.
 CC FT VARIANT 216 216 Y -> L (IN DEFECTIVE VARIANT C5D).
 CC FT VARIANT 217 1680 MISSING (IN DEFECTIVE VARIANT C5D).
 CC SQ SEQUENCE 1680 AA; 188877 MW; 81EB5A16FAC7D95C CRC64;
 CC -----
 CC Query Match 48.9%; Score 69; DB 1; Length 1680;
 CC Best Local Similarity 47.1%; Pred. No. 7,23e-04;
 CC Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 CC Rhabditidae; Peloderinae; Caenorhabditis.
 CC [1]
 CC RA SEQUENCE FROM N.A.
 CC RC STRAIN-BRISTOL N2;
 CC RA Langston Z., Mohlmann P., Gilliam B.;
 CC RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 CC CC -1- FUNCTION: INVOLVED IN PROTEIN IMPORT INTO THE MITOCHONDRION.
 CC PROBABLY INVOLVED IN TRANSLLOCATION ACROSS THE INNER MEMBRANE. AS A
 CC BINDING PROTEIN REQUIRED FOR DRIVING THE IMPORT OF PREPROTEINS.
 CC RECRUITS MITOCHONDRIAL HSP70 TO DRIVE PROTEIN TRANSLLOCATION INTO
 CC THE MATRIX USING ATP AS AN ENERGY SOURCE (BY SIMILARITY).
 CC -1- SUBUNIT: FORMS PART OF THE RECEPTOR COMPLEX THAT CONSISTS OF AT
 CC LEAST 3 DIFFERENT PROTEINS (TIM17, TIM23, TIM44) (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE (POTENTIAL).
 CC -1- SIMILARITY: BELONGS TO THE TIM44 FAMILY.
 CC -----
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 CC -----
 CC EMBL: U97405; AAB53011.1; -
 CC WORMPEP: T0984.9; CE13473.
 CC DR Mitochondrion; Inner membrane; Transport; Protein transport;
 CC KW Translocation; Translocase; Translocase; Translocase;
 CC FT TRANSIT 1 ?
 CC FT CHAIN ? 425
 CC FT SEQUENCE 425 AA; 49398 MW; 203DFBD614E099F8 CRC64;
 CC -----
 CC Query Match 42.6%; Score 60; DB 1; Length 425;
 CC Best Local Similarity 38.9%; Pred. No. 1.1e-01;
 CC Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

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QY      ||::||:| |::
       7 TKSKKCVQKVE 18

RESULT 6
ID      QVEJ_ECOLI      STANDARD;      PRT;      160 AA.
AC      Q46943; P77135;
DT      01-NOV-1997 (Rel. 35, Created)
DT      15-JUL-1998 (Rel. 36, Last sequence update)
DT      15-JUL-1998 (Rel. 36, Last annotation update)
DE      HYPONHEICAL 18.7 KDA PROTEIN IN KDU1-LYSS INTERGENIC REGION.
GN      QVEJ.
OS      Escherichia coli.
OC      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC      Escherichia.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=K12 / MG1655;
RX      MEDLINE; 97426617.
RA      Blattner F.R., Plunkett G. III, Bloch C.A., Ferna N.T., Burland V.,
RA      Riley M., Collado-Vides J., Glasner F.D., Rode C.K., Mayhew G.F.,
RA      Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA      Mau B., Shao Y.;
RA      "The complete genome sequence of Escherichia coli K-12.";
RL      Science 277:1453-1474 (1997).
RN      [2]
RP      SEQUENCE OF 34-160 FROM N.A.
RC      STRAIN=K12 / MG1655;
RA      Roberts D., Allen E., Araujo R., Aparicio A., Chung E., Davis K.,
RA      Duncan M., Fiederspiel N., Hyman R., Kalman S., Komp C., Kurdi O.,
RA      Lew H., Lin D., Namath A., Oefner P., Schramm S., Davis R.W.;
RA      Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC      -----
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CC      -----
CC      EMBL; U29581; AAB40495.1; ALT_INIT.
DR      EMBL; AE000368; AAC75887.1; ALT_INIT.
DR      EMBL; U83187; AAB40287.1; -.
DR      ECOGENE; EGI3101; yqeJ
KW      Hypothetical protein; Transmembrane.
FT      TRANSMEM 8 28 POTENTIAL.
SQ      SEQUENCE 160 AA; 18719 MW; 10910D39F2B5F70D CRC64;

Query Match      41.1%; Score 58; DB 1; Length 160;
Best Local Similarity 40.0%; Pred. No. 3; 19e-01;
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Db      74 QQGNRESKSRNRNTE 88
       :|| : || :|| :|
QY      4 HOGTKSKKCVQKVE 18

RESULT 7
ID      RL34_HUMAN      STANDARD;      PRT;      116 AA.
AC      P49207;
DT      01-FEB-1996 (Rel. 33, Created)
DT      01-FEB-1996 (Rel. 33, Last sequence update)
DT      15-FEB-2000 (Rel. 39, Last annotation update)
DE      60S RIBOSOMAL PROTEIN L34.
DE      RPL34.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=OVARY.
RX      MEDLINE; 96039267.

```

RA Rommens J.M., Durocher F., McArthur J., Tonin P., Leblanc J.F.,
 RA Allen T., Samson C., Feril L., Narod S., Morgan K., Simard J.,
 RT "Generation of a transcription map at the HSD17B locus centromeric to
 RT BRCA1 at 17q21.";
 RL Genomics 28:530-542(1995).
 RN [12]
 RP SEQUENCE OF 3-47 FROM N.A.
 RX MEDLINE; 98248690.
 RA Kenmochi N., Kawaguchi T., Rozen S., Davis E., Goodman N.,
 RA Hudson T.J., Tanaka T., Page D.C.;
 RT "A map of 75 human ribosomal protein genes.";
 RL Genome Res. 8:509-523(1998).
 CC -1- SIMILARITY: BELONGS TO THE L34E FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
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 CC -----
 CC EMBL; L38941; AAC41916.1; -
 DR EMBL; AB007181; BA25840.1; -
 DR PFM; PF01199; Ribosomal_L34e; 1.
 DR PROSITE; PS01145; RIBOSOMAL_L34E; 1.
 KM Ribosomal protein.
 FT INIT MET 0 BY SIMILARITY
 SO SEQUENCE 116 AA; 13174 MW; 0C1EBA2AAAC8A5D3 CRC64;
 Query Match 40.4%; Score 57; DB 1; Length 116;
 Best Local Similarity 41.7%; Pred. No. 5,36e-01;
 Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

DB 79 GSKACVCVRRI 90
 I:::|||||:::
 QY 6 GTRSSKCVQKRV 17

RESULT 8
 ID CSH_ARTSP STANDARD; PRT; 264 AA.
 AC P32400;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE N-CARBAMOYL-SARCOSE AMIDASE (EC 3.5.1.59) (N-CARBAMOYL-SARCOSE
 DE AMIDOHYDROLASE) (CSHASE).
 OS Arthrobacter sp.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Micrococcales; Micrococcaceae; Arthrobacter.
 RN [1]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS), AND REVISIONS TO 184 AND 232.
 RX MEDLINE; 92389321.
 RA Romao M.J., Turk D., Gomis-Rueth F.-X., Huber R.;
 RT "Crystal structure analysis, refinement and enzymatic reaction
 RT mechanism of N-carbamoylsarcosine amidohydrolase from Arthrobacter
 RT sp. at 2.0-A resolution.";
 RL J. Mol. Biol. 226:111-1130(1992).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.28 ANGSTROMS) OF COMPLEX WITH INHIBITORS.
 RX MEDLINE; 97070380.
 RA Zajc A., Romao M.J., Turk D., Huber R.;
 RT "Crystallographic and fluorescence studies of ligand binding to N-
 RT carbamoylsarcosine amidohydrolase from Arthrobacter sp.";
 RL J. Mol. Biol. 263:269-283(1996).
 CC -1- CATALYTIC ACTIVITY: N-CARBAMOYL-SARCOSE + H(2)O = SARCOSE +
 CC CO(2) + NH(3).
 CC -1- COFACTOR: ONE SULFATE ION PER SUBUNIT.
 CC -1- PATHWAY: DEGRADATION OF CREATININE TO GLYCINE.
 CC -1- SUBUNIT: HOMOTETRAMER.
 DR PIR; S28969; S28969.
 DR PDB; 1NBA; 22-JUN-94.
 DR PFM; PF00857; Isochorismatase; 1.
 RN

KM Hydrolase; 3D-structure.
 FT ACT_SITE 177 177 INVOLVED IN HYDROLYSIS OF THE SUBSTRATE.
 SQ SEQUENCE 264 AA; 29057 MW; 8A213B555EA5DCDC CRC64;
 Query Match 40.4%; Score 57; DB 1; Length 264;
 Best Local Similarity 40.0%; Pred. No. 5,36e-01;
 Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

DB 171 GATAGCVRRTVEDA 185
 I:::|||||:::
 QY 6 GTRSSKCVQKKEGS 20

RESULT 9
 ID IT16_ARATH STANDARD; PRT; 89 AA.
 AC O22869;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE PURATIVE TRYPSIN INHIBITOR T01024.29 PRECURSOR.
 GN T01024.29.
 GN Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; Rosidae; eurosids II; Brassicales;
 OC Brassicaceae; Arabidopsis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLOMBIA;
 RA Roundley S.D., Tschudy M.M., Lin X., Ketchum K.A., Crosby M.L.,
 RA Brandon R.C., Spriggs T.A., Mason T.M., Kertlavage A.R., Adams M.D.,
 RA Somerville C.R., Venter J.C.;
 RL Submitted (Jul-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE RT1/MTI-2 PROTEASE INHIBITORS FAMILY.
 CC -----
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 CC -----
 CC EMBL; AC002335; AAB64322.1; -
 DR Serine protease inhibitor; Signal; Multigene family.
 KM SIGNAL 1 26
 FT CHAIN 27 89 POTENTIAL.
 FT DISULFID 33 86 POTATIVE TRYPSIN INHIBITOR T01024.29.
 FT DISULFID 46 70 BY SIMILARITY.
 FT DISULFID 55 81 BY SIMILARITY.
 FT DISULFID 59 83 BY SIMILARITY.
 FT ACT_SITE 49 50 REACTIVE-BOND (BY SIMILARITY).
 SQ SEQUENCE 89 AA; 10192 MW; C0964810F3099A3 CRC64;
 Query Match 39.7%; Score 56; DB 1; Length 89;
 Best Local Similarity 60.0%; Pred. No. 8,95e-01;
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

DB 64 GAKGKCVQK 73
 I:::|||||:::
 QY 6 GTRSSKCVQK 15

RESULT 10
 ID SP70_DICDI STANDARD; PRT; 537 AA.
 AC P15269; P08126;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE SPORE COAT PROTEIN SP70 PRECURSOR (BREJIN PROTEIN).
 GN COTB.
 GN Dictyostelium discoideum (slime mold).
 OC Eukaryota; Dictyostelida; Dictyostelium.
 RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE; 90097939.
RA Fornaugh K.L., Loomis W.F.;
RT "Spore coat genes SP60 and SP70 of Dictyostellium discoideum.";
RN J. Cell Biol. 9:5215-5218(1989).
RN [2]
RP PRELIMINARY SEQUENCE OF 72-170 FROM N.A.
RX MEDLINE; 87057653.
RA Gomer R.H., Datta S., Firtel R.A.;
RT "Cellular and subcellular distribution of a cAMP-regulated prestalk
protein and prespore protein in Dictyostellium discoideum: a study on
the ontogeny of prestalk and prespore cells.";
RL J. Cell Biol. 103:1999-2015(1986).
CC -!- PTM: PHOSPHORYLATED AND FUCOSYLATED.
CC -!- SIMILARITY: CONTAINS 3 PRESPORE MOTIFS.
CC -----
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CC -----
CC EMBL; M26238; AAA33252.1; -.
CC DR M26238; AAA33252.1; -.
CC DR PIR; B33485; B33485.
CC DR PIR; B25439; B25439.
CC DR DICTYDB; DD03009; COTB.
KW Glycoprotein; Phosphorylation; Repeat; Sporulation; Signal.
FT SIGNAL 1 20
FT CHAIN 21 537 SPORE COAT PROTEIN SP70.
FT DOMAIN 182 250 SER/THR-RICH.
FT DOMAIN 190 248 5.5 X 11 AA TANDEM REPEATS.
FT REPEAT 190 200 1.
FT REPEAT 191 211 2.
FT REPEAT 212 222 3.
FT REPEAT 223 233 4.
FT REPEAT 234 244 5.
FT REPEAT 245 248 6 (INCOMPLETE).
FT REPEAT 251 263 PRESPORE MOTIF 1.
FT REPEAT 279 291 PRESPORE MOTIF 2.
FT REPEAT 359 371 PRESPORE MOTIF 3.
FT CARBOHYD 97 POTENTIAL.
SQ SEQUENCE 537 AA; 56650 MW; 0EA20BDC96DE2A19 CRC64;

Query Match 39.7%; Score 56; DB 1; Length 537;
Best Local Similarity 54.5%; Pred. No. 8.95e-01;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 291 KNGECIRDKVE 301
|:|:|:|:|
QY 8 KSSKCVQRKVE 18

RESULT 11
ID GLB1-MAIZE STANDARD; PRT; 573 AA.
AC P15590;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE GLOBULIN-1 S ALLELE PRECURSOR (GLB1-S) (7S-LIKE).
GN GLB1.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. INBRED LINE VA26;
RA Belanger F.C., Kriz A.L.;
RT "Molecular characterization of the major maize embryo globulin encoded
by the Glb1 gene.";
RL Plant Physiol. 91:636-643(1989).
RN [2]

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RP SEQUENCE OF 87-100.
RX MEDLINE; 89374022.
RA Kriz A.L.;
RT "Characterization of embryo globulins encoded by the maize Glb
genes.";
RL Biochem. Genet. 27:239-251(1989).
CC -!- PTM: THREE PROTEIN-PROCESSING STEPS OCCUR IN THE FORMATION OF THE
MATURE PROTEIN FROM THE PRIMARY TRANSLATION PRODUCT.
CC -!- POLYMORPHISM: THE THREE MOST COMMONLY OCCURRING GLB1 ALLELES HAVE
THE DESIGNATION L, I, AND S FOR LARGE, INTERMEDIATE, AND SMALL
PROTEINS, RESPECTIVELY.
CC -!- SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASEOLIN, VICILIN,
CONVICILIN, CONGLYCININ, ETC.).
CC -----
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CC -----
CC EMBL; M24845; AAA33467.1; -.
CC DR HSSP; P50477; ICAN.
CC DR MAIZEDB; 30181; -.
CC DR PFAM; PF00546; Seedstore_7s; 1.
KW Seed storage protein; Signal. OR 21 (POTENTIAL).
FT SIGNAL 1 18
FT PROPEP 19 86
FT CHAIN 87 573 GLOBULIN-1 S ALLELE.
FT CARBOHYD 349 349 POTENTIAL.
SQ SEQUENCE 573 AA; 65029 MW; 525EDID00A062976 CRC64;

Query Match 39.7%; Score 56; DB 1; Length 573;
Best Local Similarity 58.3%; Pred. No. 8.95e-01;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 32 HGGHSGRCVRR 43
|:|:|:|:|
QY 4 HGGTSSKCVQRQ 15

RESULT 12
ID RPOB_PSEPU STANDARD; PRT; 1357 AA.
AC P19175;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE DNA-DIRECTED RNA POLYMERASE BETA CHAIN (PC 2.7.7.6) (TRANSCRIPTASE
BETA CHAIN) (RNA POLYMERASE BETA SUBUNIT).
GN RPOB.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
OC Pseudomonas.
RN [1]
RP SEQUENCE FROM N.A.
RA Borodin A.M., Danilkovich A.V., Allikmets R.L., Rostapshov V.M.,
RA Chernov I.P., Azhikina T.L., Monastyrskaya S., Sverdlov D.;
RT "Nucleotide sequence of the rpoB gene coding for the beta-subunit of
RNA polymerase in Pseudomonas putida.";
RL Dokl. Biochem. 302:1261-1265(1988).
RN [2]
RP SEQUENCE OF 1036-1357 FROM N.A.
RX MEDLINE; 89117617.
RA Borodin A.M., Danilkovich A.V., Chernov I.P., Azhikina T.L.,
RA Rostapshov V.M., Monastyrskaya G.S.;
RT "Genes coding for RNA polymerase in bacteria. III. The use of
modified Sanger's method for sequencing the C-terminal region of rpoB
gene, N-terminal region of rpoC gene and intercistron region of RNA
polymerase in Pseudomonas putida.";
RL Bioorg. Khim. 14:1179-1182(1988).
CC -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS

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CC SUBSTRATES.
 CC -1- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE +
 CC RNA(N).
 CC -1- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
 CC ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
 CC BETA' CHAIN.
 CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
 CC -----
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 CC -----
 CC EMBL: X15849; CAA33846.1; -;
 CC DR EMBL: M38319; AAA25986.1; -;
 CC DR PIR: P00362; RNA_POL_B; 1.
 CC DR PROSITE: PS01166; RNA_POL_BETA; 1.
 CC FT Transferrase; Transcription; DNA-directed RNA polymerase.
 CC FT CONFLICT 1180 1180 T -> N (IN REF. 2).
 CC FT CONFLICT 1184 1184 I -> V (IN REF. 2).
 CC FT CONFLICT 1236 1236 F -> S (IN REF. 2).
 CC SQ SEQUENCE 1357 AA; 151305 MW; 4AEDB68CB086EA6 CRC64;

Query Match 39.7%; Score 56; DB 1; Length 1357;
 Best Local Similarity 41.2%; Pred. No. 8,956-01;

Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Db 450 IDHGNRRVRCVGEAE 466

OY 2 IDHGRKSKCVROKVE 18

RESULT 13
 AC YTX1_XENLA STANDARD; PRT; 775 AA.
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-APR-1990 (Rel. 14, Last annotation update)
 DE TRANSDON TXI HYPOTHETICAL 82 KDA PROTEIN (OFR 1).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC Xenopodinae; Xenopus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 89384562.
 RA Garrett J.E., Knutson D.S., Carroll D.;
 RT *Composite transposable elements in the Xenopus laevis genome.*;
 RL Mol. Cell. Biol. 9:3018-3027(1989).
 CC -----
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 CC -----
 CC EMBL: M26915; AAA49975.1; -;
 CC DR PIR: A32494; A32494.
 CC DR PRINTS: PR00939; C2HCZNFINGER.
 CC KW Hypothetical protein; Transposable element.
 CC SQ SEQUENCE 775 AA; 82355 MW; B8C361AEC65DD85B CRC64;

Query Match 39.0%; Score 55; DB 1; Length 775;
 Best Local Similarity 46.7%; Pred. No. 1,486+00;

Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Db 617 SNTSKVSSEVEGAP 631

||||| |||:

OY 7 TKSSKCVROKVEGSS 21

RESULT 14
 AC COT2_BACSU STANDARD; PRT; 148 AA.
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE SPORE COAT PROTEIN 2.
 GN COT2.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-168 / JH642;
 RX MEDLINE: 93285989.
 RA Zhang J., Fitz-James P.C., Aronson A.I.;
 RT Cloning and characterization of a cluster of genes encoding
 RT polypeptides present in the insoluble fraction of the spore coat of
 RT Bacillus subtilis.
 RL J. Bacteriol. 173:3757-3766(1993).
 CC -1- SUBUNIT: DISULFIDE CROSS-LINKED EITHER TO ITSELF OR TO COTY.
 CC -1- SUBCELLULAR LOCATION: SPORE OUTER COAT.
 CC -1- SIMILARITY: TO COTY.
 CC -----
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 CC -----
 CC EMBL: L10116; AAA22329.1; -;
 CC DR EMBL: 299110; CAB13031.1; -;
 CC DR PIR: FA7119; E47119.
 CC DR SUBTILIST; BG10439; COT2.
 CC KW Sporulation.
 CC SQ SEQUENCE 148 AA; 16534 MW; 90429FFB050896E CRC64;

Query Match 38.3%; Score 54; DB 1; Length 148;
 Best Local Similarity 63.6%; Pred. No. 2,446+00;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 4 KTSKCVREAVE 14

OY 8 KSKCVROKVE 18

RESULT 15
 AC R1B7_METJA STANDARD; PRT; 224 AA.
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE PUTATIVE 5-AMINO-6-(5-PHOSPHORIBOSYLAMINO)URACIL REDUCTASE
 DE (EC 1.1.1.193) (HTP REDUCTASE).
 GN Mj0671.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
 OC Methanococcus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE: 96337999.
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
 RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii.";
RL Science 273:1058-1073(1996).
CC -!- CATALYTIC ACTIVITY: 5-AMINO-6-(5-PHOSPHORIBITYLAMINO)URACIL +
CC NADP(+) = 5-AMINO-6-(5-PHOSPHORIBOSYLAMINO)URACIL + NADPH.
CC -!- PATHWAY: THIRD STEP OF RIBOFLAVIN BIOSYNTHESIS.
CC -!- SIMILARITY: BELONGS TO THE HTP REDUCTASE FAMILY.
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CC -----
DR EMBL; U67514; AAB98665.1; -.
DR TIGR; MJ0671; -.
DR PFAM; PF01872; RibD_C; 1.
KW Hypothetical protein: Riboflavin biosynthesis; Oxidoreductase; NADP.
SQ SEQUENCE 224 AA; 25037 MW; 4D8C15CE291E89D8 CRC64;

Query Match 38.3%; Score 54; DB 1; Length 224;
Best Local Similarity 33.3%; Pred. No. 2.44e+00;
Matches 6; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Db 118 ILEDMGVEVVKCGRGVD 135
::: | || | | |
QY 1 VIDHQGTKSKCVQRKVE 18

Search completed: Wed Sep 6 08:15:32 2000
Job time : 12 secs.

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 (TM)

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Msprch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Sep 6 08:15:49 2000; Maspar time 6.73 Seconds 216.433 Million cell updates/sec

Tabular output not generated.

Title: >US-08-487-283A-1
 Description: (1-21) from US08487283A.pep
 Perfect Score: 141
 Sequence: 1 VIDHGTGKSKVCVRQKVEGSS 21

Scoring table: PAM 150
 Gap 15

Searched: 225878 segs, 69334122 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: spiremb112
 1:sp-archaea 2:sp-bacteria 3:sp-fungi 4:sp-human
 5:sp-invertebrate 6:sp-mammal 7:sp-mhc 8:sp-organelle
 9:sp-phage 10:sp-plant 11:sp-rodent 12:sp-unclassified
 13:sp-invertebrate 14:sp-virus

Statistics: Mean 25.849; Variance 31.531; scale 0.820

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	68	48.2	936	2	Q9ZKD6	PUTATIVE CYTOCHROME C- 8.98e-03
2	65	46.1	936	2	Q25141	CYTOCHROME C BIOGENESI 7.25e-02
3	64	45.4	543	2	Q9X7U3	PUTATIVE PROTEASE 1.21e-01
4	63	44.7	213	10	Q41275	TRANSCRIPTION FACTOR S 2.00e-01
5	62	44.0	213	2	Q53550	HYPOTHETICAL 22.7 KD P 3.31e-01
6	61	43.3	214	10	Q64645	MADS BOX PROTEIN AG120 5.44e-01
7	60	42.6	1166	5	Q96219	HYPOTHETICAL 139.4 KD 8.88e-01
8	59	41.8	940	2	Q51187	LACTOFERRIN BINDING PR 8.88e-01
9	59	41.8	943	2	Q87343	LACTOFERRIN BINDING PR 8.88e-01
10	59	41.8	943	2	Q50952	LACTOFERRIN RECEPTOR 8.88e-01
11	58	41.1	205	11	Q60969	PROTEIN TYROSINE PHOSP 1.44e+00
12	58	41.1	223	11	Q60970	PROTEIN TYROSINE PHOSP 1.44e+00
13	58	41.1	259	2	P71852	HYPOTHETICAL 26.8 KD P 1.44e+00
14	58	41.1	451	5	P90814	F46C5.9 PROTEIN. 1.44e+00
15	58	41.1	972	5	Q26614	FIBROBLAST GROWTH FACT 1.44e+00
16	57	40.4	963	4	Q34829	KIAA0724 PROTEIN. 2.33e+00
17	56	39.7	80	14	Q84420	A99L PROTEIN. 3.75e+00
18	56	39.7	236	10	Q81250	GLOBULIN-1 (FRAGMENT) 3.75e+00
19	56	39.7	236	10	Q81254	GLOBULIN-1 (FRAGMENT) 3.75e+00
20	56	39.7	238	10	Q81257	GLOBULIN-1 (FRAGMENT) 3.75e+00

21	56	39.7	238	10	Q81255	GLOBULIN-1 (FRAGMENT) 3.75e+00
22	56	39.7	238	10	Q81249	GLOBULIN-1 (FRAGMENT) 3.75e+00
23	56	39.7	240	10	Q81252	GLOBULIN-1 (FRAGMENT) 3.75e+00
24	56	39.7	240	10	Q81256	GLOBULIN-1 (FRAGMENT) 3.75e+00
25	56	39.7	242	10	Q81251	GLOBULIN-1 (FRAGMENT) 3.75e+00
26	56	39.7	407	10	Q41750	GLOBULIN-1 (FRAGMENT) 3.75e+00
27	56	39.7	453	5	Q44021	CORONIN. 3.75e+00
28	56	39.7	540	10	Q03866	GLOBULIN-1 S ALLELE PR 3.75e+00
29	56	39.7	809	10	Q03866	SUCROSE SYNTHASE (EC 2 3.75e+00
30	55	39.0	153	2	Q53889	CHROMOSOME PRE-INITIAT 6.00e+00
31	55	39.0	504	1	Q29585	MED10-CHAIN ACT1-COA 6.00e+00
32	55	39.0	510	5	Q62120	CC4.3 PROTEIN. 6.00e+00
33	55	39.0	565	5	Q9X334	LAMIN. 6.00e+00
34	55	39.0	1053	14	Q9M502	MAJOR OUTER CAPSID PRO 6.00e+00
35	55	39.0	1349	5	Q62613	NUCLEOPORIN. 6.00e+00
36	55	39.0	1365	5	Q62610	NUCLEOPORIN. 6.00e+00
37	55	39.0	1365	5	Q62536	NUCLEOPORIN. 6.00e+00
38	55	39.0	2967	14	Q41892	POLYPROTEIN PRECURSOR. 6.00e+00
39	54	38.3	249	10	Q24234	M79 PROTEIN. 9.52e+00
40	54	38.3	259	10	Q24229	MADS BOX PROTEIN. 9.52e+00
41	54	38.3	1030	3	Q12180	CHROMOSOME XV READING 9.52e+00
42	54	38.3	1097	2	P72196	TONB-LINKED ADHESIN PR 9.52e+00
43	54	38.3	1732	2	Q07442	LYSINE-SPECIFIC CYSTEI 9.52e+00
44	54	38.3	1732	2	Q52050	LYSINE SPECIFIC CYSTEI 9.52e+00
45	54	38.3	2470	11	Q35516	CELL SURFACE PROTEIN. 9.52e+00

ALIGNMENTS

RESULT ID	1	PRELIMINARY;	PRT;	936 AA.
AC	Q9ZKD6;			
DT	01-MAY-1999 (TREMBLrel. 10, Created)			
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)			
DT	01-MAY-1999 (TREMBLrel. 10, Last annotation update)			
DE	PUTATIVE CYTOCHROME C-TYPE BIOGENESIS PROTEIN.			
GN	JHP1003.			
OS	Helicobacter pylori J99.			
OC	Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group; Helicobacter.			
RN	SEQUENCE FROM N.A.			
RP	STRAIN-J99;			
RC	MEDLINE: 99120557.			
RX	ALM R.A., LING L.S.L., MOIR D.T., KING B.L., BROWN E.D., DOIG P.C., SMITH D.R., NOONAN B., GUILD B.C., DEJONGE B.L., CARMEL G., TUDMINO P.J., CARUSO A., URIA-NICKELSEN M., MILLS D.M., IVES C., GIBSON R., MERBERG D., MILLS S.D., JIANG Q., TAYLOR D.E., VOYTS G.F., TRUST T.J.;			
RA	"Genomic-sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";			
RT	Nature 397:176-180(1999).			
RL	EMBL: AE001528; AAD06582.1;			
DR	SEQUENCE 936 AA; 106452 MW; A43D80C0 CRC32;			
DB	366 IDMHGSAKIERKIENPA 385			
QY	2 IDHGTGKSKVCVRQKVEGSS 21			
Query Match	48.2%;	Score 68;	DB 2;	Length 936;
Best Local Similarity	50.0%;	Pred. No. 8.98e-03;		
Matches	10;	Conservative 5;	Mismatches 5;	Indels 0;
Gaps	0;			
RESULT ID	2	PRELIMINARY;	PRT;	936 AA.
AC	Q25141.			
DT	01-JAN-1998 (TREMBLrel. 05, Created)			
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)			
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)			
DE	CYTOCHROME C BIOGENESIS PROTEIN (YCF5).			
GN	HP0378.			
OS	Helicobacter pylori (Campylobacter pylori).			


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RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-PCC6803;
RX MEDLINE: 97061201.
RA KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
RA MIYAJIMA N., HIROKAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
RA HOSOUCHI T., MATSUO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S.,
RA SHIMO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
RA TABATA S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
DR EMBL: D63999; BAA10048.1; -.
KW Hypothetical protein.
SQ SEQUENCE 213 AA; 22745 MW; 88506910 CRC32;

Query Match 44.0%; Score 62; DB 2; Length 213;
Best Local Similarity 35.0%; Pred. No. 2.00e-01;
Matches 7; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Db 92 ILAYIGAKASDCIKPKYVSS 111
OY 1 VIDHGTSSKCVKQKEGS 20

RESULT 6 PRELIMINARY; PRT; 214 AA.
ID 064645;
AC 064645;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE MADS BOX PROTEIN AG120.
GN MADS OR F17K2.19.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA;
RA ROUNSELEY S.D., KAUL S., LIN X., KETCHUM K.A., CROSBY M.L.,
RA BRANON R.C., SYKES S.M., MASON T.M., KERLAVAGE A.R., ADAMS M.D.,
RA SOMERVILLE C.R., VENTER J.C.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS A DOMAIN FOUND IN SRF-TYPE TRANSCRIPTION
CC FACTORS (MADS-DOMAIN).
DR EMBL: AC003680; AAC06175.1; -.
DR HSSP: P11746; 1MAN.
DR MENDEL; 29412; Arabid; MADS; 29412.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PFAM; PF01486; K-box; 1.
DR PFAM; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
KW Transcription regulation; DNA-binding; Nuclear protein.
SQ SEQUENCE 214 AA; 24533 MW; E2D3914C CRC32;

Query Match 43.3%; Score 61; DB 10; Length 214;
Best Local Similarity 46.7%; Pred. No. 3.31e-01;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Db 127 IEQQLERSVRCIRAR 141
OY 2 IDHGTSSKCVKQKEGS 16

RESULT 7 PRELIMINARY; PRT; 1166 AA.
ID 096219;
AC 096219;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)

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DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE HYPOTHETICAL 139.4 KD PROTEIN.
GN PFB0630C.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 99021743.
RA GARDNER M.J., TETTELIN H., CARUCCI D.J., CUMMINGS L.M., ARAYIND L.,
RA KOONIN E.V., SHALLON S., MASON T., YU K., FUJI C., PEDERSON J.,
RA SHEN K., JING J., ASTON C., LAI Z., SCHWARTZ D.C., PERTER M.,
RA SALZBERG S., ZHOU L., SUTTON G.G., CLAYTON R., WHITE O., SMITH H.O.,
RA FRASER C.M., ADAMS M.D., VENTER J.C., HOFFMAN S.L.;
RT "Chromosome 2 sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Science 282:1126-1132(1998).
DR EMBL: AE001407; AAC71915.1; -.
KW Hypothetical protein.
SQ SEQUENCE 1166 AA; 139389 MW; D72D31F8 CRC32;

Query Match 42.6%; Score 60; DB 5; Length 1166;
Best Local Similarity 43.8%; Pred. No. 5.44e-01;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Db 611 EHRGKKEKCVTKIIE 626
OY 3 DHGTSSKCVKQKEGS 18

RESULT 8 PRELIMINARY; PRT; 940 AA.
ID 051187;
AC 051187;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE LACTOFERRIN BINDING PROTEIN.
GN LBPA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-H44/76;
RX MEDLINE: 9527374.
RA PETERSSON A.M., KLARENBEK V., VAN DEUREN J., POOLMAN J.T.,
RA TOMMASEN J.;
RL "Molecular characterization of the structural gene for the lactoferrin
RT receptor of the meningococcal strain H44/76.";
RL Microb. Pathog. 17:395-408(1994).
DR EMBL: X79838; CAA56233.1; -.
DR PFAM; PF00593; TOMB_BOX; 1.
DR SEQUENCE 940 AA; 105347 MW; 01ACA021 CRC32;

Query Match 41.8%; Score 59; DB 2; Length 940;
Best Local Similarity 50.0%; Pred. No. 8.88e-01;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 592 RSRKCVPRKINSN 605
OY 8 KSKCVKQKEGS 21

RESULT 9 PRELIMINARY; PRT; 943 AA.
ID 087343;
AC 087343;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE LACTOFERRIN BINDING PROTEIN A PRECURSOR.
GN LBPA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=DNM2;
RX MEDLINE; 98261564.
RA LEWIS L.A., ROHDE K., GIPSON M., BEHRENS B., GRAY E., TOTH S.I.,
RA ROE B.A., DYER D.W.;
RT "Identification and molecular analysis of lbpA, which encodes the
RT two-component meningococcal lactoferrin receptor.";
RL Infect. Immun. 66:3017-3023(1998).
DR EMBL; AF049349; AAC35271.1; -.
DR PFAM; PF00593; TonB_boxC; 1.
KW Signal.
FT SIGNAL 1 24
FT CHAIN 24 943 LACTOFERRIN BINDING PROTEIN A.
SQ SEQUENCE 943 AA; 105426 MW; 087E2FC6 CRC32;

Query Match 41.8%; Score 59; DB 2; Length 943;
Best Local Similarity 50.0%; Pred. No. 8.88e-01;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 595 RSRKCVPRKINGSN 608
QY 8 KSSKCVQRKVEGSS 21

RESULT 10
ID Q50952 PRELIMINARY; PRT; 943 AA.
AC Q50952;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE LACTOFERRIN RECEPTOR PRECURSOR.
GN LBPA.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=FA19;
RC MEDLINE; 95347808.
RA BISWAS G.D., SPARLING P.F.;
RT "Characterization of lbpA, the structural gene for a lactoferrin
RT receptor in Neisseria gonorrhoeae.";
RL Infect. Immun. 63:2958-2967(1995).
CC -1- SIMILARITY: STRONG, TO N.MENINGITIDIS IRON-REGULATED OUTER
CC MEMBRANE PROTEIN A.
CC
DR EMBL; U16260; RAC13780.1; -.
DR PFAM; PF00593; TonB_boxC; 1.
KW Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 943 LACTOFERRIN RECEPTOR.
SQ SEQUENCE 943 AA; 105669 MW; 4D8AF2C4 CRC32;

Query Match 41.8%; Score 59; DB 2; Length 943;
Best Local Similarity 50.0%; Pred. No. 8.88e-01;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 595 RSRKCVPRKINGSN 608
QY 8 KSSKCVQRKVEGSS 21

RESULT 11
ID Q50969 PRELIMINARY; PRT; 205 AA.
AC Q50969;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE PROTEIN TYROSINE PHOSPHATASE-LIKE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-SKELETAL MUSCLE;
MEDLINE; 96070766.

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RA WISHART M.J., DENU J.M., WILLIAMS J.A., DIXON J.E.;
RT "A single mutation converts a novel phosphotyrosine binding domain
RT into a dual-specificity phosphatase.";
RL J. Biol. Chem. 270:26782-26785(1995).
DR EMBL; U34973; AAA87036.1; -.
DR HSSP; P51452; 1VHR.
DR PFAM; PF00782; DSPC; 1.
SQ SEQUENCE 205 AA; 23683 MW; 7B70331A CRC32;

Query Match 41.1%; Score 58; DB 11; Length 205;
Best Local Similarity 25.0%; Pred. No. 1.44e+00;
Matches 5; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Db 51 ILQKHGITHIICIRONIAN 70
QY 1 VIDHOGTKSSKCVQRKVEGS 20

RESULT 12
ID Q60970 PRELIMINARY; PRT; 223 AA.
AC Q60970;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE PROTEIN TYROSINE PHOSPHATASE-LIKE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-SKELETAL MUSCLE;
MEDLINE; 96070766.
RA WISHART M.J., DENU J.M., WILLIAMS J.A., DIXON J.E.;
RT "A single mutation converts a novel phosphotyrosine binding domain
RT into a dual-specificity phosphatase.";
RL J. Biol. Chem. 270:26782-26785(1995).
DR EMBL; U34973; AAA87037.1; -.
DR HSSP; P51452; 1VHR.
DR PFAM; PF00782; DSPC; 1.
SQ SEQUENCE 223 AA; 25416 MW; 7D7F6D83 CRC32;

Query Match 41.1%; Score 58; DB 11; Length 223;
Best Local Similarity 25.0%; Pred. No. 1.44e+00;
Matches 5; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Db 51 ILQKHGITHIICIRONIAN 70
QY 1 VIDHOGTKSSKCVQRKVEGS 20

RESULT 13
ID P71852 PRELIMINARY; PRT; 259 AA.
AC P71852;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE HYPOTHETICAL 26.8 KD PROTEIN.
GN MTCY03C7.07.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RA SKELTON J., CHURCHER C.M.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RA BARRELL B.G., RAJANDREAM M.A.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.

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 NWSETH

 (TM)

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MSrch.p protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Sep 6 08:17:17 2000; Maspar time 2.98 seconds

Tabular output not generated. 166,869 Million cell updates/sec

Title: >US-08-487-283A-1
 Description: (1-21) from US08487283A.pep
 Perfect Score: 141
 Sequence: 1 VIDHOGTKSSKCVRKVEGSS 21

Scoring table: PAM 150
 Gap 15

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: a-geneseq36
 1:geneseqp

Statistics: Mean 18.949; Variance 55.942; scale 0.339

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	141	100.0	21	R77605	Pro-C5 polypeptide KSS	1.94e-09
2	141	100.0	1676	R77604	Pro-C5 polypeptide.	1.94e-09
3	57	40.4	117	R707037	Breast cancer associat	3.93e+01
4	55	39.0	264	R22271	CSHase.	6.46e+01
5	54	38.3	249	W84049	Rice OsmAD57 protein 1	8.26e+01
6	54	38.3	1732	W69487	Haemagglutinin protein	8.26e+01
7	54	38.3	1732	W24787	Prk antigenic protein	8.26e+01
8	54	38.3	1732	R96029	P. gingivalis porphyrin	8.26e+01
9	54	38.3	3163	R94347	Hepatitis GB virus (HG	8.26e+01
10	53	37.6	589	R14327	Mouse epithelial precu	1.05e+02
11	53	37.6	589	W85474	Mouse GP88 autocrine g	1.05e+02
12	53	37.6	652	R88124	Tobacco mosaic virus r	1.05e+02
13	53	37.6	1009	R26206	Type B human platelet-	1.05e+02
14	53	37.6	1089	R08267	Platelet derived grovt	1.05e+02
15	53	37.6	1089	R06910	Alpha type PDGF recept	1.05e+02
16	53	37.6	1196	W04326	Rat perlin.	1.05e+02
17	52	36.9	14	W85479	Mouse GP88 autocrine g	1.34e+02
18	52	36.9	99	W5446	Mouse novel secreted p	1.34e+02
19	52	36.9	99	W5762	Human HDCAp protein.	1.34e+02
20	52	36.9	186	W40824	Mycobacterium tubercul	1.34e+02
21	52	36.9	248	W84050	Rice OsmAD58 protein 1	1.34e+02
22	52	36.9	354	R33439	Ornithine cyclodextrina	1.34e+02
23	52	36.9	455	W76439	Human p53 regulated pr	1.34e+02

24	52	36.9	593	1	W62835	26a mays antimicrobial	1.34e+02
25	51	36.2	511	1	W78475	Autographa californica	1.71e+02
26	51	36.2	530	1	W78476	Baculovirus ISP protei	1.71e+02
27	51	36.2	589	1	R14325	Rat epithelial precurs	1.71e+02
28	51	36.2	637	1	W64388	A. thaliana SGT protei	1.71e+02
29	51	36.2	674	1	W64389	A. thaliana protein co	1.71e+02
30	51	36.2	707	1	W36064	Rat neurodap 1 protein	1.71e+02
31	51	36.2	730	1	Y00191	Enterococcus faecalis	1.71e+02
32	51	36.2	764	1	Y00190	Enterococcus faecalis	1.71e+02
33	51	36.2	914	1	R15785	B. thuringiensis toxin/	1.71e+02
34	51	36.2	956	1	R15784	B. thuringiensis toxin/	1.71e+02
35	51	36.2	986	1	R25141	JAK2.	1.71e+02
36	51	36.2	1100	1	R15783	B. thuringiensis toxin/	1.71e+02
37	51	36.2	1129	1	R70830	Murine JAK2 kinase.	1.71e+02
38	51	36.2	1144	1	R88122	Tobacco mosaic virus r	1.71e+02
39	51	36.2	1144	1	R88123	Tobacco mosaic virus r	1.71e+02
40	51	36.2	1588	1	R46605	Malariat PTEM3 epitop	1.71e+02
41	51	36.2	1663	1	R46608	Plasmodium falciparum	1.71e+02
42	50	35.5	37	1	W98577	H. pylori GPO 37 prot	2.17e+02
43	50	35.5	422	1	W56275	Flavobacterium keratol	2.17e+02
44	50	35.5	446	1	W69563	Sugarbeet choline mono	2.17e+02
45	50	35.5	1047	1	W01535	Cellular homologue of	2.17e+02

ALIGNMENTS

RESULT	1
ID	R77605 standard; Protein: 21 AA.
AC	R77605;
DT	02-APR-1996 (first entry)
DE	Pro-C5 polypeptide KSSK epitope.
KW	Complement C5; haemolysis; kidney; glomerulonephritis;
KW	monoclonal antibody; antinflammatory; antibody engineering;
KW	humanised antibody; KSSK epitope.
OS	Homo sapiens.
PN	W09529697-A1.
PD	09-NOV-1995.
PF	01-MAY-1995: U05688.
PR	02-MAY-1994: US-236208.
PA	(ALEX-) ALEXION PHARM INC.
PI	Evans MJ, Matlis L, Mueller EE, Nye SH, Rollins S;
PI	Rother RP, Springhorn J P, Squinto SP, Thomas TC;
PI	Wang Y, Wilkins JA;
DR	WPI: 95-392923/50.
PT	Treating glomerulonephritis with antibody against complement C5
PT	Component - to inhibit complement induced cell lysis
PS	Example 13, Page 81; 18pp; English.
CC	The CDNA sequence of the complement C5 gene transcript predicts a
CC	secreted pro-C5 precursor of 1676 amino acids (R77604). C5 is a
CC	beta-globulin heterodimer thought to play a role in the pathogenesis
CC	of glomerulonephritis (GN). Cleavage of the C5 alpha-chain
CC	by a convertase enzyme generates anaphylatoxic C5a. Monoclonal
CC	and humanised recombinant antibodies that recognise the alpha-chain
CC	KSSK epitope (R77605) block C5a generation, thereby reducing
CC	glomerular inflammation and kidney dysfunction associated with GN.
CC	Sequence 21 AA;
SO	
Query Match	100.0%; Score 141; DB 1; Length 21;
Best Local Similarity	100.0%; Pred. No. 1.94e-09;
Matches	21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB	1 VIDHOGTKSSKCVRKVEGSS 21
OY	1 VIDHOGTKSSKCVRKVEGSS 21
RESULT	2
ID	R77604 standard; Protein: 1676 AA.
AC	R77604;
DT	15-MAR-1996 (first entry)
DE	Pro-C5 polypeptide.
KW	Complement C5; haemolysis; kidney; glomerulonephritis;
KW	monoclonal antibody; antinflammatory; antibody engineering;


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KW humanised antibody.
OS Homo sapiens.
FH Key Location/Qualifiers
FT peptide 1..18 /label= Sig_peptide
FT protein 19..673 /label= Beta-chain
FT cleavage_site 673..674 /label= Cleavage_peptide
FT cleavage_site 677..678 /label= Alpha-chain
FT peptide 674..677 /note= "amino acids 872-892 (854-874 of
FT protein label= Cleavage_peptide the mature protein) comprise the KSSKS
FT 678..1676 epitope"
FT peptide 678..751 /label= c5a
FT cleavage_site 751..752 /label= Convertase_cleavage_site
FT modified_site 911 /label= N-glycosylation_site
FT modified_site 1115 /label= N-glycosylation_site
FT modified_site 1630 /label= N-glycosylation_site
FT WO9529697-A1.
PN 09-NOV-1995.
PD 01-MAY-1995; US-5688.
PF 02-MAY-1994; US-236208.
PR (ALEX-) ALEXION PHARM INC.
PA Evans MJ, Matlis L, Mueller EE, Nye SH, Rollins S;
PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;
PI Wang Y, Wilkins JA;
PI WPI; 95-392923/50.
DR Treating glomerulonephritis with antibody against complement C5
PT component - to inhibit complement induced cell lysis
PS Example 13; Page 82-92; 181pp; English.
CC The cDNA sequence of the complement C5 gene transcript predicts a
CC secreted pro-C5 precursor of 1676 amino acids (R77604). C5 is a
CC beta-globulin heterodimer thought to play a role in the pathogenesis
CC of glomerulonephritis (GN). Cleavage of the C5 alpha-chain
CC by a convertase enzyme generates anaphylatoxic C5a. Monoclonal
CC and humanised recombinant antibodies that recognise the alpha-chain
CC KSSKC epitope (R77605) block C5a generation, thereby reducing
CC glomerular inflammation and kidney dysfunction associated with GN.
CC Sequence 1676 AA;
SQ
Query Match 100.0%; Score 141; DB 1; Length 1676;
Best Local Similarity 100.0%; Pred. No. 1.94e-09;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 872 VIDHOGTKSSKCVQRKVEGSS 892
QY 1 VIDHOGTKSSKCVQRKVEGSS 21

RESULT 3
ID Y07037 standard; Protein; 117 AA.
AC Y07037;
DT 02-JUL-1999 (first entry)
DE Breast cancer associated antigen precursor sequence.
KW Cancer associated antigen; diagnosis; research; treatment; human;
KW breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
KW prostate cancer.
OS Homo sapiens.
PN WO9904265-A2.
PD 28-JAN-1999.
PF 15-JUL-1998; U14679.
PR 22-JUN-1998; US-102322.
PR 17-JUL-1997; US-896164.
PR 10-OCT-1997; US-061599.
PR 10-OCT-1997; US-061765.

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PR 10-OCT-1997; US-948705.
PR 11-OCT-1997; GB-021697.
PA (LUDW-) LUDWIG INST CANCER RES.
PI Chen Y, Gout I, Gure A, Ohare M, Obata Y, Old LJ,
PI Pfeundschn M, Sahin U, Scanlan MJ, Stockert E,
PI Tureci O;
PI WPI; 99-132448/11.
DR New isolated cancer associated nucleic acids and polypeptides -
PT isolated using sera from cancer patients, used to develop products
PT for the diagnosis, monitoring or treatment of cancers
PT Disclosure; Page 422; 787pp; English.
PS The invention relates to a method for diagnosing a disorder characterised
CC by expression of a human cancer associated antigen precursor coded for by
CC a nucleic acid molecule (NAM). The method comprises: (a) contacting a
CC biological sample isolated from a subject with an agent that specifically
CC binds to the NAM, an expression product or a fragment of an expression
CC product complexed with an HLA molecule; and (b) determining the
CC interaction between the agent and the NAM or the expression product as a
CC determination of the disorder. The products and methods can be used in
CC the diagnosis, monitoring, research, or treatment of conditions
CC characterised by the expression of various cancer associated antigens.
CC The invention provides nucleic acid sequences and encoded polypeptides
CC which are cancer associated antigen precursors expressed in human breast
CC cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
CC lung cancer.
SQ Sequence 117 AA;

Query Match 40.4%; Score 57; DB 1; Length 117;
Best Local Similarity 41.7%; Pred. No. 3.93e-01;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Db 80 GSMCAKCVEDRI 91
QY 6 GTRSKCVQRKV 17
|:::|||||:::

RESULT 4
ID R22271 standard; Protein; 264 AA.
AC R22271;
DT 30-JUL-1992 (first entry)
DE CSHase.
KW N-carbamoyl-sarcosine amidohydrolase; CSH; assay; diagnosis;
KW creatinine.
OS Arthrobacter sp. DSM 2563.
PN Ep-476670-A.
PD 25-MAR-1992.
PF 19-SEP-1991; 115974.
PR 20-SEP-1990; DE-029844.
PA (BOEF) BOEHRINGER MANNHEIM GMBH.
PI Burtcher H, Schumacher G;
PI WPI; 92-098378/13.
DR N-PSDB; Q22713.
PT Recombinant DNA encoding N-carbamoyl-sarcosine-amidohydrolase -
PT useful in clinical assay of creatinine, and vectors providing
PT efficient expression in E.coli
PS Claim 9; Page 9 + 7; 12pp; German.
CC The sequence encoding CSHase is useful in assay of creatinine
CC (for diagnosis of kidney disease). It can now be prep. more
CC simply than by known methods which involve culture of Arthrobacter
CC on complex media.
SQ Sequence 264 AA;

Query Match 39.0%; Score 55; DB 1; Length 264;
Best Local Similarity 46.2%; Pred. No. 6.46e-01;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 171 GATACGVRHVE 183
QY 6 GTRSKCVQRKV 18
|:::|||||:::

RESULT 5
ID W84049 standard; Protein; 249 AA.

```

[illegible]

Best Local Similarity 31.6%; Pred. No. 8.26e+01;
Matches 6; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Db 1097 ITAGVRSKPAIRGRIQGT 1115

QY 2 IDHQGTKSKCVRKVEGS 20

RESULT 8

ID R96029 standard; Protein; 1732 AA.

AC R96029;

DT 04-SEP-1996 (first entry)

DE P. gingivalis porphyain.

OS Porphyain; haemagglutinin; periodontal disease; vaccine; antibody.

KW Porphyromonas gingivalis strain W12.

FT Key Location/Qualifiers

FT region 688..708

FT /note= "Pro-Asn repeat region type 1"

FT region 887..952

FT /note= "Pro-Asn repeat region type 2"

FT region 946..967

FT /note= "Pro-Asn repeat region type 1"

FT region 985..1006

FT /note= "Pro-Asn repeat region type 2"

FT region 1041..1100

FT /note= "Pro-Asn repeat region type 3"

FT region 1341..1405

FT /note= "Pro-Asn repeat region type 4"

FT region 1430..1451

FT /note= "Pro-Asn repeat region type 2"

FT region 1488..1547

FT /note= "Pro-Asn repeat region type 3"

FT region 1607..1650

FT /note= "Pro-Asn repeat region type 4"

FT /note= "Pro-Asn repeat region type 2"

PN W09617936-A2.

PD 13-JUN-1996.

PF 11-DEC-1995; U16108.

PR 09-DEC-1994; US-353485.

PA (UABR-) UAB RES FOUND.

PA (UFL) UNIV FLORIDA.

PI Han N, Lantz M, Lepine G, Patti JM, Progulake-Fox A;

PI Tumwasorn S;

DR WPI: 96-287181/29.

DR N-PSDB: T30653.

PT Porphyromonas gingivalis genes and proteins - used in the detection

PT and vaccination against periodontal disease

PS Claim 5; Page 76-81; 153pp; English.

CC P. gingivalis W12 cysteine protease, porphyain (R96029), was

CC identified as the product of the prp gene (T30653) isolated from

CC P. gingivalis W12 genomic DNA. The porphyain shows homology to

CC the haemagglutinins (see also R96026-28 and R96030-33) of P.

CC gingivalis 318. It can be obtd. from transformed host cells and

CC used as a vaccine to protect humans or animals against periodontal

CC disease. Expression in Salmonella cells allows prodn. of a live

CC vaccine. The porphyain and haemagglutinins can also be used to

CC detect the presence of anti-P. gingivalis antibodies and to raise

CC monoclonal antibodies for diagnostic appln.

SQ Sequence 1732 AA;

Query Match 38.3%; Score 54; DB 1; Length 1732;

Best Local Similarity 31.6%; Pred. No. 8.26e+01;

Matches 6; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Db 1097 ITAGVRSKPAIRGRIQGT 1115

QY 2 IDHQGTKSKCVRKVEGS 20

RESULT 9

ID R94347 standard; Protein; 3163 AA.

AC R94347;

DT 02-JUL-1996 (first entry)

DE Hepatitis GB virus (HGBV) clone GB contig A protein prod.

KW Hepatitis GB virus; HGBV; diagnosis; treatment; vaccine;
KW reagents; non-A; non-B; non-C; non-D; non-E; clone; GB contig A;
KW tamarin; infected plasma; lambda phage; cDNA library.

OS Hepatitis GB virus.

FT Key Location/Qualifiers

FT misc_difference 1..3163

FT /note= "others correspond to degenerate or STOP

FT codons in T00129"

PN W09521922-A2.

PD 17-AUG-1995.

PF 14-FEB-1995; U02118.

PR 14-FEB-1994; US-196030.

PR 13-MAY-1994; US-242654.

PR 29-JUL-1994; US-283314.

PR 23-NOV-1994; US-344190.

PR 23-NOV-1994; US-344185.

PR 27-JAN-1995; US-344557.

PA (ABSO) ABBOTT LAB.

PI Buijk SL, Dawson GJ, Desai SM, Erker JC, Leary TP;

PI Muerthoff AS, Mushahwar IK, Pilot-Matias TJ, Schlauder GG;

PI Simons JN;

DR WPI: 95-293123/38.

DR N-PSDB; T00129.

PT Non-A, non-B, non-C, non-D, non-E Hepatitis virus reagents - useful

PT for diagnosis and therapy of hepatitis GB virus

PS Example 9; Pages 401-414; 661pp; English.

CC Double stranded hepatitis GB virus (HGBV) DNA obtd. from HGBV

CC infected tamarin plasma, using standard procedures, was used to

CC prepare a lambda phage HGBV cDNA library. Clones were rescued

CC from the lambda phage, searched against a sequence database and

CC found to be unique HGBV sequences. The clones were then used to

CC assemble the sequences T00129/30 (GB contig A and B) which encode

CC the proteins R94345-47 (the 3 possible coding strand reading

CC frames) and R82072, respectively. Reagents which comprise the HGBV

CC DNA, or its protein prods. can be used for the diagnosis, therapy

CC or in a vaccine to prevent HGBV infection.

SQ Sequence 3163 AA;

Query Match 38.3%; Score 54; DB 1; Length 3163;

Best Local Similarity 40.0%; Pred. No. 8.26e+01;

Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Db 528 VVDORPLKGCVCVRD 542

QY 1 VIDHQGTKSKCVRQ 15

RESULT 10

ID R14327 standard; Protein; 589 AA.

AC R14327;

DT 17-JAN-1992 (first entry)

DE Mouse epithelin precursor.

KW ET; growth regulation; inhibition; stimulation.

OS Mus musculus.

FT Key Location/Qualifiers

FT protein 1..589

FT /label= precursor

FT /note= "claim 21, page 55"

FT 280..335

FT /label= Ep-1

FT /note= "claim 22, page 55"

FT protein 205..261

FT /label= Ep-2

FT /note= "claim 23, page 55"

FT peptide 59..114

FT /label= Ep

FT /note= "claim 24, page 55"

FT peptide 123..179

FT /label= Ep

FT /note= "claim 25, page 55"

FT peptide 362..416

FT /label= Ep

FT /note= "claim 26, page 56"


```
FT protein /label= Signal_peptide
FT 24. .1009
FT /label= Mature PDGF-A
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Query Match      37.6%; Score 53; DB 1; Length 1009;
Best Local Similarity 38.1%; Pred. No. 1.05e-02;
Matches      8; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Db      381  VDDHGSTGGTGTCTAECTP 401
QY      1  VIDHQGTKSKCVRQKVEGSS 21

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Query Match 37.6%; Score 53; DB 1: Length 1089;
Best Local Similarity 38.1%; Pred. No. 1.05e-02;
Matches 8; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
Db .421 VDDHGGSTGGQTVRCCTAECTP 441

QY 1 |||: :: || |||:
1 VIDHGTKSKCKVRQKEGGS 21

RESULT 15

ID R06910 standard; protein; 1089 AA.
AC R06910;
DE 16-JAN-1991 (first entry)
DE Alpha type PDGF receptor deduced from TR4 cDNA clone.
DE Platelet derived growth factor; T11.
OS Homo sapiens.
FH Key Location/Qualifiers
FT domain 1..23
FT FT /label=signal peptide
FT domain 24..524
FT FT /label=ligand binding domain
FT domain 525..548
FT FT /label=transmembrane region
FT domain 549..599
FT FT /label=juxtamembrane domain
FT binding_site 600..627
FT FT /label-ATP binding site
FT modified_site 849
FT FT /label-tyrosine autophosphorylation site
FT modified_site 42..44
FT FT /label-N-glycos_site
FT modified_site 76..78
FT FT /label-N-glycos_site
FT modified_site 103..105
FT FT /label-N-glycos_site
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FT modified_site 359..361
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FT modified_site 458..460
FT FT /label-N-glycos_site
FT modified_site 468..470
FT FT /label-N-glycos_site
PN W09010013-A.
PD 07-SEP-1990.
PD 08-FEB-1990; U00617.
PR 09-FEB-1989; US-308282.
PA (USDC) US SEC OF COMMERCE
PI Matsui T, Aaronson SA, Pierce JH;
DI WPI; 90-290306/38.
DR NP-SDB; Q05989.
DR Type alpha platelet-derived growth factor receptor gene
PT for transforming cells to express novel protein receptor
PT susceptible to genetic engineering.
PS Claim 7; Fig 3; 64pp; English.
CC The TR4 clone is the largest cDNA clone related to the TR
CC clone, isolated from a library prep'd. from human thymus I
CC T4 cDNA clone was isolated from a M426 human embryo fibro
CC cDNA library. The coding region can be introduced into
CC gpt vector with a simian sarcoma virus LTR as a promoter
CC expressed in a host. The resulting protein is a novel
CC receptor designated type alpha (the known receptor is des
CC type beta). The polypeptide has a calculated molecular m
CC kd and has all the characteristics of a membrane spann
CC kinase receptor. The extracellular region comprises a h
CC signal peptide and a ligand binding domain which has str
CC homology with the PDGF-R/CsF1-R subfamily. Ten Cys resi
CC spaced at the same positions as in other receptors of the
CC family and eight potential N-linked glycosylation sites
CC present. A hydrophobic segment spans the membrane and th
CC plasmaic region comprises a juxtamembrane region, a tyros
CC region split into TK1 and TK2 by a hydrophilic interkin
CC and a hydrophilic C-terminal tail. The TK region includ
CC consensus ATP binding sequence (G-X-G-X-G...K) and a
CC autophosphorylation site homologous to that of pp60(v-sr
CC Sequence 1089;AA:
CC

Query Match 37.6%; Score 53; DB 1; Length 1089;
Best Local Similarity 38.1%; Pred. No. 1.05e+02;
Matches 8; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

DB 421 VDDHGSTGGGTVRCTAAGTP 441

QY 1 VIDHGTSSKCVRQKVEGSS 21

Search completed: Wed Sep 6 08:17:28 2000
Job time : 11 secs.

MORSE
***** (TM)

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MPsrch.p protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Sep 6 08:17:46 2000; Maspar time 2.27 Seconds

Tabular output not generated. 141.637 Million cell updates/sec

Title: >US-08-487-283A-1
Description: (1-21) from US08487283A.pep
Perfect Score: 141
Sequence: 1 VIDHGTSSKRCVROKVEGSS 21

Scoring table: PAM 150
Gap 15

Searched: 152433 seqs, 15329240 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5A_COMB 2:5B_COMB 3:6_COMB 4:PCT_COMB 5:backfiles1

Statistics: Mean 17.928; Variance 54.211; scale 0.331

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	59	41.8	944	2	US-08-867-Sequence 23, Applicat	1.44e+01
2	59	41.8	944	2	US-08-867-Sequence 24, Applicat	1.44e+01
3	58	41.1	24	2	US-08-827-Sequence 127, Applicat	1.85e+01
4	58	41.1	24	1	US-08-484-Sequence 127, Applicat	1.85e+01
5	58	41.1	24	2	US-08-484-Sequence 127, Applicat	1.85e+01
6	55	39.0	264	1	US-08-107-Sequence 2, Applicatio	3.90e+01
7	54	38.3	249	2	US-08-867-Sequence 15, Applicati	4.99e+01
8	54	38.3	1732	2	US-08-353-Sequence 10, Applicati	4.99e+01
9	54	38.3	1732	2	US-08-570-Sequence 6, Applicatio	6.38e+01
10	53	37.6	589	2	US-08-431-Sequence 6, Applicatio	6.38e+01
11	53	37.6	589	2	US-08-431-Sequence 6, Applicatio	6.38e+01
12	53	37.6	589	2	US-08-429-Sequence 6, Applicatio	6.38e+01
13	53	37.6	589	2	US-07-668-Sequence 6, Applicatio	6.38e+01
14	53	37.6	652	4	PCT-US95-0-Sequence 6, Applicatio	6.38e+01
15	53	37.6	652	4	US-08-261-Sequence 6, Applicatio	6.38e+01
16	53	37.6	1089	3	US-08-462-Sequence 2, Applicatio	6.38e+01
17	53	37.6	1089	4	PCT-US92-0-Sequence 4, Applicatio	6.38e+01
18	53	37.6	1089	4	US-08-475-Sequence 36, Applicati	6.38e+01
19	53	37.6	1089	2	US-08-475-Sequence 36, Applicati	6.38e+01
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21	53	37.6	1089	3	US-08-460-Sequence 4, Applicatio	6.38e+01
22	53	37.6	1089	1	US-08-168-Sequence 4, Applicatio	6.38e+01
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25	53	37.6	1089	1	US-08-180-Sequence 36, Applicati	6.38e+01
26	53	37.6	1143	2	US-08-310-Sequence 108, Applicat	6.38e+01
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29	53	37.6	1144	4	PCT-US95-0-Sequence 2, Applicatio	6.38e+01
30	53	37.6	1144	1	US-08-261-Sequence 4, Applicatio	6.38e+01
31	53	37.6	1144	1	US-08-261-Sequence 4, Applicatio	6.38e+01
32	52	36.9	99	2	US-08-795-Sequence 1, Applicatio	8.13e+01
33	52	36.9	186	2	US-08-655-Sequence 15, Applicati	8.13e+01
34	52	36.9	186	2	US-08-655-Sequence 2, Applicatio	8.13e+01
35	52	36.9	248	2	US-08-667-Sequence 17, Applicati	8.13e+01
36	52	36.9	3177	2	US-08-477-Sequence 4, Applicatio	8.13e+01
37	51	36.2	530	3	US-09-105-Sequence 2, Applicatio	1.04e+02
38	51	36.2	589	2	US-08-431-Sequence 2, Applicatio	1.04e+02
39	51	36.2	589	2	US-08-429-Sequence 2, Applicatio	1.04e+02
40	51	36.2	993	1	US-08-446-Sequence 25, Applicati	1.04e+02
41	51	36.2	1129	4	PCT-US95-1-Sequence 9, Applicatio	1.04e+02
42	51	36.2	1129	1	US-08-097-Sequence 9, Applicatio	1.04e+02
43	51	36.2	1129	1	US-08-357-Sequence 6, Applicatio	1.04e+02
44	51	36.2	1129	2	US-09-003-Sequence 6, Applicatio	1.04e+02
45	51	36.2	1663	4	PCT-US93-0-Sequence 16, Applicati	1.04e+02

ALIGNMENTS

RESULT	1	STANDARD:	PRT:	944 AA.
ID	US-08-867-941-23			
AC	xxxxxx			
DT				
XX				

Sequence 23, Application US/08867941

Sequence 23, Application US/08867941

Patent No. 5977337

GENERAL INFORMATION:

APPLICANT: Loosmore, Sheena M

APPLICANT: Du, Run-Pan

APPLICANT: Wang, Qiljun

APPLICANT: Yang, Yan-Ping

APPLICANT: Kiehl, Michel H

TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA

NUMBER OF SEQUENCES: 67

CORRESPONDENCE ADDRESSES:

ADDRESS: 6th Floor, 330 University Avenue

CITY: Toronto

STATE: Ontario

COUNTRY: Canada

ZIP: M5G 1R7

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/867,941

FILING DATE: 03-JUN-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Stewart, Michael I

REGISTRATION NUMBER: 24,973

REFERENCE/DOCKET NUMBER: 1038-681 MIS:jb

TELECOMMUNICATION INFORMATION:

TELEPHONE: (416) 595-1155

TELEFAX: (416) 595-1163

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 944 amino acids

TYPE: amino acid

STRANDEDNESS: single


```

DE Sequence 127, Application US/08484635
xx
cc Sequence 127, Application US/08484635
cc Patent No. 5773569
cc GENERAL INFORMATION:
cc APPLICANT: Wrighton, Nicholas C.
cc APPLICANT: Dower, William J.
cc APPLICANT: Chang, Ray S.
cc APPLICANT: Kashyap, Atun K.
cc APPLICANT: Jolliffe, Linda K.
cc APPLICANT: Mulcahy, Linda
cc APPLICANT: Johnson, Dana
cc TITLE OF INVENTION: Compounds and Peptides That Bind to the
cc TYPE OF INVENTION: Erythropoietin Receptor
cc NUMBER OF SEQUENCES: 259
cc CORRESPONDENCE ADDRESS:
cc ADDRESSEE: Townsend and Crew
cc STREET: One Market Plaza, Stewart Street Tower
cc CITY: San Francisco
cc STATE: California
cc COUNTRY: USA
cc ZIP: 94105-1492
cc COMPUTER READABLE FORM:
cc MEDIUM TYPE: Floppy disk
cc COMPUTER: IBM PC compatible
cc OPERATING SYSTEM: PC-DOS/MS-DOS
cc SOFTWARE: Patentin Release #1.0, Version #1.30
cc CURRENT APPLICATION DATA:
cc APPLICATION NUMBER: US/08/484,635
cc FILING DATE: 07-JUN-1995
cc CLASSIFICATION: 514
cc PRIOR APPLICATION DATA:
cc APPLICATION NUMBER: US 08/155,940
cc FILING DATE: 19-NOV-1993
cc ATTORNEY/AGENT INFORMATION:
cc NAME: Garrett-Wackowski, Eugenia
cc REGISTRATION NUMBER: 37,330
cc REFERENCE/DOCKET NUMBER: 16528A-43-1-1
cc TELECOMMUNICATION INFORMATION:
cc TELEPHONE: (415) 543-9600
cc TELEFAX: (415) 543-5043
cc INFORMATION FOR SEQ ID NO: 127:
cc SEQUENCE CHARACTERISTICS:
cc LENGTH: 24 amino acids
cc TYPE: amino acid
cc STRANDEDNESS:
cc TOPOLOGY: linear
cc MOLECULE TYPE: peptide
cc SEQUENCE 24 AA: 2547 MW: 2814 CN:
SQ
Query Match 41.1%; Score 58; DB 1; Length 24;
Best Local Similarity 46.7%; Pred.NO. 1.85e+01;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0.
Db 10 GQKTPCVRRRLG 24
0Y 5 GQTKSSKCVRKVEG 19
RESULT 5 STANDARD; PRT; 24 AA.
xx US-08-484-631-127
xx AC xxxxxx
xx DN
xx DE Sequence 127, Application US/08484631
xx Sequence 127, Application US/08484631
xx Patent No. 5830851
xx GENERAL INFORMATION:
xx APPLICANT: Wrighton, Nicholas C.
xx APPLICANT: Dower, William J.
xx

```

CC	APPLICANT:	Chang, Ray S.
CC	APPLICANT:	Kashyap, Arun K.
CC	APPLICANT:	Jolliffe, Linda K.
CC	APPLICANT:	Johnson, Dana
CC	APPLICANT:	Mulcahy, Linda
CC	TITLE OF INVENTION:	Compounds and Peptides That Bind to the
CC	TITLE OF INVENTION:	Erythropoietin Receptor
CC	NUMBER OF SEQUENCES:	259
CC	CORRESPONDENCE ADDRESS:	
CC	ADDRESSEE:	Townsend and Townsend and Crew
CC	STREET:	One Market Plaza, Stewart Street Tower
CC	CITY:	San Francisco
CC	STATE:	California
CC	COUNTRY:	USA
CC	ZIP:	94105-1492
CC	COMPUTER READABLE FORM:	
CC	MEDIUM TYPE:	Floppy disk
CC	COMPUTER:	IBM PC compatible
CC	OPERATING SYSTEM:	PC-DOS/MS-DOS
CC	SOFTWARE:	PatentIn Release #1.0, Version #1.30
CC	CURRENT APPLICATION DATA:	
CC	APPLICATION NUMBER:	US/08/484,631
CC	FILING DATE:	07-JUN-1995
CC	CLASSIFICATION:	514
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER:	US 08/155,940
CC	FILING DATE:	19-NOV-1993
CC	ATTORNEY/AGENT INFORMATION:	
CC	NAME:	Garrett-Wackowski, Eugenia
CC	REGISTRATION NUMBER:	37,330
CC	REFERENCE/DOCKET NUMBER:	16528A-43-1-2
CC	TELECOMMUNICATION INFORMATION:	
CC	TELEPHONE:	(415) 543-9600
CC	TELEFAX:	(415) 543-5043
CC	INFORMATION FOR SEQ ID NO:	127:
CC	SEQUENCE CHARACTERISTICS:	
CC	LENGTH:	24 amino acids
CC	TYPE:	amino acid
CC	STRANDEDNESS:	
CC	TOPOLOGY:	linear
CC	MOLECULE TYPE:	peptide
CC	SEQUENCE	24 AA; 2547 MW; 2614 CN;
DB	Query Match	41.1%; Score 58; DB 2; Length 24; Best Local Similarity 46.7%; Pred.No.1.85e+01;
OY	Matches	Similarity 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
Db	10 OGPRTWPCVRRRLGG 24 : : 5 OGRTSSKCVFKVEG 19	
RESULT	6	
ID	US-08-107-042-2	STANDARD; PRT; 264 AA.
XX AC	xxxxxx	
DT		
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DE	Sequence 2, Application US/08107042	
XX	Sequence 2, Application US/08107042	
CC	Patent No. 5416014	
CC	GENERAL INFORMATION:	
CC	APPLICANT:	Butscher, Helmut
CC	APPLICANT:	Schumacher, Gunther
CC	TITLE OF INVENTION:	CLONED N-CARBAMOYL SARCOSINE
CC	TITLE OF INVENTION:	AMIDOHYDROLASE
CC	NUMBER OF SEQUENCES:	3
CC	CORRESPONDENCE ADDRESS:	
CC	ADDRESSEE:	Armstrong, Nikolaïd, Marmelstein, Kubovcik &
CC	ADDRESSEE:	MurRAY
CC	STREET:	1725 K Street N.W., Suite 1000

CC	CITY:	Washington D.C.
CC	COUNTRY:	United States of America
CC	ZIP:	20006
CC	COMPUTER READABLE FORM:	
CC	MEDIUM TYPE:	Floppy disk
CC	COMPUTER:	IBM PC compatible
CC	OPERATING SYSTEM:	PC-DOS/MS-DOS
CC	SOFTWARE:	PatentIn Release #1.0, Version #1.25
CC	CURRENT APPLICATION DATA:	
CC	APPLICATION NUMBER:	US/08/107,042
CC	FILING DATE:	
CC	CLASSIFICATION:	435
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER:	US/07/762,131
CC	FILING DATE:	
CC	APPLICATION NUMBER:	DE P 40 29 844.2
CC	FILING DATE:	20-SEP-1990
CC	ATTORNEY/AGENT INFORMATION:	
CC	NAME:	Murray, Robert B.
CC	REGISTRATION NUMBER:	22,890
CC	REFERENCE/DOCKET NUMBER:	911286
CC	TELECOMMUNICATION INFORMATION:	
CC	TELEPHONE:	202-659-2930
CC	TELEFAX:	202-887-0357
CC	TELEX:	440142
CC	INFORMATION FOR SEQ ID NO: 2:	
CC	SEQUENCE CHARACTERISTICS:	
CC	LENGTH:	264 amino acids
CC	TYPE:	amino acid
CC	TOPOLOGY:	linear
CC	MOLECULE TYPE:	protein
CC	SEQUENCE	264 AA; 29153 MW; 361847 CN;
SS	Query Match	39.0%; Score 55; DB 1; Length 264;
	Best Local Similarity	46.2%; Pred.No. 3.90e+01;
	Matches	6; Conservative 4; Mismatches 3; Indels 0;
Db	171	GATAAGCVRHTVE 183
QY	5	GTKSKCKVRQKVE 18
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RESULT	7	
ID	US-08-867-087B-15	STANDARD: - PRT: 249 AA.
XX	xxxxxx	
AC		
XX		
DT		
XX		
DE	Sequence 15, Application US/08867087B	
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CC	Sequence 15, Application US/08867087B	
CC	Patent No. 5990386	
CC	GENERAL INFORMATION:	
CC	APPLICANT:	An, Gynheung
CC	TITLE OF INVENTION:	GENES CONTROLLING FLORAL DEVELOPMENT
CC	TITLE OF INVENTION:	AND APICAL DOMINANCE IN PLANTS
CC	NUMBER OF SEQUENCES:	70
CC	CORRESPONDENCE ADDRESS:	
CC	ADDRESSEE:	Klarquist Sparkman Campbell Leigh &
CC	ADDRESSEE:	Whinston, LLP
CC	STREET:	One World Trade Center
CC	STREET:	121 S.W. Salmon Street
CC	STREET:	Suite 1600
CC	CITY:	Portland
CC	STATE:	Oregon
CC	COUNTRY:	United States of America
CC	ZIP:	97204
CC	COMPUTER READABLE FORM:	
CC	MEDIUM TYPE:	Disk, 3-1/2 inch
CC	COMPUTER:	IBM PC compatible
CC	OPERATING SYSTEM:	MS DOS
CC	SOFTWARE:	WordPerfect 5.1

CC	CURRENT APPLICATION DATA:
CC	APPLICATION NUMBER: US/08/867,087B
CC	FILING DATE: June 2, 1997
CC	CLASSIFICATION: 800
CC	PRIOR APPLICATION DATA:
CC	APPLICATION NUMBER: U.S. 08/323,449
CC	FILING DATE: October 14, 1994
CC	APPLICATION NUMBER: U.S. 08/485,981
CC	FILING DATE: June 7, 1995
CC	ATTORNEY/AGENT INFORMATION:
CC	NAME: Dow, Alan E.
CC	REGISTRATION NUMBER: 35,123
CC	REFERENCE/DOCKET NUMBER: 4630-47071
CC	TELECOMMUNICATION INFORMATION:
CC	TELEPHONE: (503) 226-7391
CC	TELEFAX: (503) 228-9446
CC	INFORMATION FOR SEQ ID NO: 15:
CC	SEQUENCE CHARACTERISTICS:
CC	LENGTH: 249 amino acid residues
CC	TYPE: amino acid
CC	TOPOLOGY: linear
CC	SEQUENCE 249 AA; 28682 MW; 300604 CN;
QY	Query Match 38.3%; Score 54; DB 2; Length 249; Best Local Similarity 26.3%; Pred. No. 4.99e+01; Matches 5; Conservative 10; Mismatches 4; Indels 0; Gaps 0;
Db	160 EQMVSEANRCLRRKLEESN 178 :: : :: : : : :
QY	3 DHOGTKSKCVQRKEGSS 21
RESULT	8
ID	US-08-353-485-10 STANDARD; PRT; 1732 AA.
XX	xxxxxx
AC	
XX	
DT	
XX	
DE	Sequence 10, Application US/08353485
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CC	Sequence 10, Application US/08353485
CC	Patent No. 5830710
CC	GENERAL INFORMATION:
CC	APPLICANT: Proguiske-Fox, Ann
CC	APPLICANT: Tumwasorn, Somying
CC	APPLICANT: Lepine, Guylaine
CC	APPLICANT: Han, Naiming
CC	APPLICANT: Lantz, Marilyn
CC	APPLICANT: Patti, Joseph
CC	TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
CC	TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
CC	NUMBER OF SEQUENCES: 12
CC	CORRESPONDENCE ADDRESS:
CC	ADDRESSEE: Ted W. Whitlock
CC	STREET: 2421 N.W. 41st Street, Suite A-1
CC	CITY: Gainesville
CC	STATE: FL
CC	COUNTRY: USA
CC	ZIP: 32606
CC	COMPUTER READABLE FORM:
CC	MEDIUM TYPE: Floppy disk
CC	COMPUTER: IBM PC compatible
CC	OPERATING SYSTEM: PC-DOS/MS-DOS
CC	SOFTWARE: Patentin Release #1.0, Version #1.25
CC	CURRENT APPLICATION DATA:
CC	APPLICATION NUMBER: US/08/353,485
CC	FILING DATE: 09-DEC-1994
CC	CLASSIFICATION: 424
CC	PRIOR APPLICATION DATA:
CC	APPLICATION NUMBER: US 07/647,119
CC	FILING DATE: 25-JAN-1991
CC	CLASSIFICATION: 424

CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/241,640
CC FILING DATE: 08-SEP-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Whitlock, Ted W.
CC REGISTRATION NUMBER: 36,965
CC REFERENCE/DOCKET NUMBER: UF15.C2
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (904) 375-8100
CC TELEFAX: (904) 372-5800
CC INFORMATION FOR SEQ ID NO: 10:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1732 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 1732 AA; 187874 MW; 16128552 CN;

Query Match 38.3%; Score 54; DB 2; Length 1732;
Best Local Similarity 31.6%; Pred. No. 4.99e+01;
Matches 6; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Db 1097 ITAKGVSPKAIKRGRIQT 1115
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QY 2 IDHGTGKSKVCVQKVEGS 20

RESULT 9
ID US-08-570-311-10 STANDARD; PRT; 1732 AA.
XX
AC xxxxxx
XX
DT
DE
XX
Sequence 10, Application US/08570311
XX
CC Sequence 10, Application US/08570311
CC Patent No. 5824791
CC GENERAL INFORMATION:
CC APPLICANT: Proguiske-Fox, Ann
CC APPLICANT: Tumwasorn, Somying
CC APPLICANT: Lepine, Guylaine
CC APPLICANT: Han, Naiming
CC APPLICANT: Lantz, Marilyn
CC APPLICANT: Patti, Joseph
CC TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
CC TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
CC NUMBER OF SEQUENCES: 29
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Ted W. Whitlock
CC STREET: 2421 N.W. 41st Street, Suite A-1
CC CITY: Gainesville
CC STATE: FL
CC COUNTRY: USA
CC ZIP: 32606
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/570,311
CC FILING DATE:
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/353,485
CC FILING DATE: 09-DEC-1994
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/647,119
CC FILING DATE: 25-JAN-1991
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/241,640
CC FILING DATE: 08-SEP-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Whitlock, Ted W.
CC REGISTRATION NUMBER: 36,965
CC REFERENCE/DOCKET NUMBER: UF15.C3
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (904) 375-8100
CC TELEFAX: (904) 372-5800
CC INFORMATION FOR SEQ ID NO: 10:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1732 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 1732 AA; 187874 MW; 16128552 CN;

Query Match 38.3%; Score 54; DB 2; Length 1732;
Best Local Similarity 31.6%; Pred. No. 4.99e+01;
Matches 6; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Db 1097 ITAKGVSPKAIKRGRIQT 1115
| :|:| :|:|:|
QY 2 IDHGTGKSKVCVQKVEGS 20

RESULT 10
ID US-08-431-333-6 STANDARD; PRT; 589 AA.
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AC xxxxxx
XX
DT
DE
XX
Sequence 6, Application US/08431333
XX
CC Sequence 6, Application US/08431333
CC Patent No. 5965723
CC GENERAL INFORMATION:
CC APPLICANT: Shoyad, Mohammed
CC APPLICANT: Plowman, Gregory D.
CC TITLE OF INVENTION: EPIITHELINS: NOVEL CYSTEINE-RICH GROWTH
CC TITLE OF INVENTION: MODULATING PROTEINS
CC NUMBER OF SEQUENCES: 12
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Pennie & Edmonds
CC STREET: 1155 Avenue of the Americas
CC CITY: New York
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 10036
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/431,333
CC FILING DATE: 27-APR-1995
CC CLASSIFICATION: 536
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/668,648
CC FILING DATE: 13-MAR-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Mistock, S. Leslie
CC REGISTRATION NUMBER: 18,872
CC REFERENCE/DOCKET NUMBER: 5624-161-999
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212) 790-9090
CC TELEFAX: (212) 869-9741
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 589 amino acids
CC TYPE: amino acid

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CC      TOPOLOGY: linear
CC      MOLECULE TYPE: protein
SQ      SEQUENCE 589 AA; 63501 MW; 1690383 CN;

Query Match      37.6%; Score 53; DB 2; Length 589;
Best Local Similarity 35.7%; Pred. No. 6.38e+01;
Matches      5; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Db 560 HCSARGTKCLRKKI 573
QY 4 HOGTKSSKCVRKV 17
      | : : : : | : | :
      | : : : : | : | :

RESULT 11
ID PCT-US91-02321-6 STANDARD; PRT; 589 AA.
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AC xxxxxx
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DT
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DE Sequence 6, Application PC/TUS9102321
XX
CC      SEQUENCE 6, Application PC/TUS9102321
CC      GENERAL INFORMATION:
CC      APPLICANT: Shoyab, Mohammed
CC      APPLICANT: PLOWMAN, Gregory D.
CC      TITLE OF INVENTION: EPITHELIALS: NOVEL CYSTEINE-RICH GROWTH
CC      TITLE OF INVENTION: MODULATING PROTEINS
CC      NUMBER OF SEQUENCES: 12
CC      CORRESPONDENCE ADDRESS:
CC      ADDRESS: Bristol-Myers Squibb Company
CC      STREET: 3005 First Avenue
CC      CITY: Seattle
CC      STATE: Washington
CC      COUNTRY: USA
CC      ZIP: 98121
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Floppy disk
CC      COMPUTER: IBM PC compatible
CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      SOFTWARE: Patentin Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: PCT/US91/02321
CC      FILING DATE: 19910403
CC      CLASSIFICATION: 514
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: POOR, Brian W.
CC      REGISTRATION NUMBER: 32,928
CC      REFERENCE/DOCKET NUMBER: ON0071A-PC
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: (206)728-4800
CC      TELEFAX: (206)448-4775
CC      INFORMATION FOR SEQ ID NO: 6:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 589 amino acids
CC      TYPE: AMINO ACID
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: protein
SQ      SEQUENCE 589 AA; 63501 MW; 1690383 CN;

Query Match      37.6%; Score 53; DB 4; Length 589;
Best Local Similarity 35.7%; Pred. No. 6.38e+01;
Matches      5; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Db 560 HCSARGTKCLRKKI 573
QY 4 HOGTKSSKCVRKV 17
      | : : : : | : | :
      | : : : : | : | :

RESULT 12
ID US-08-429-998-6 STANDARD; PRT; 589 AA.
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AC xxxxxx
XX
DT
DE
DE Sequence 6, Application PC/TUS9102321
XX
CC      SEQUENCE 6, Application PC/TUS9102321
CC      GENERAL INFORMATION:
CC      APPLICANT: Shoyab, Mohammed
CC      APPLICANT: PLOWMAN, Gregory D.
CC      TITLE OF INVENTION: EPITHELIALS: NOVEL CYSTEINE-RICH GROWTH
CC      TITLE OF INVENTION: MODULATING PROTEINS
CC      NUMBER OF SEQUENCES: 12
CC      CORRESPONDENCE ADDRESS:
CC      ADDRESS: Bristol-Myers Squibb Company
CC      STREET: 3005 First Avenue
CC      CITY: Seattle
CC      STATE: Washington
CC      COUNTRY: USA
CC      ZIP: 98121
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Floppy disk
CC      COMPUTER: IBM PC compatible
CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      SOFTWARE: Patentin Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: PCT/US91/02321
CC      FILING DATE: 19910403
CC      CLASSIFICATION: 514
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: POOR, Brian W.
CC      REGISTRATION NUMBER: 32,928
CC      REFERENCE/DOCKET NUMBER: ON0071A-PC
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: (206)728-4800
CC      TELEFAX: (206)448-4775
CC      INFORMATION FOR SEQ ID NO: 6:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 589 amino acids
CC      TYPE: AMINO ACID
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: protein
SQ      SEQUENCE 589 AA; 63501 MW; 1690383 CN;

Query Match      37.6%; Score 53; DB 2; Length 589;
Best Local Similarity 35.7%; Pred. No. 6.38e+01;
Matches      5; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Db 560 HCSARGTKCLRKKI 573
QY 4 HOGTKSSKCVRKV 17
      | : : : : | : | :
      | : : : : | : | :

RESULT 13
ID US-07-668-648-6 STANDARD; PRT; 589 AA.
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AC xxxxxx
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DT
DE
DE Sequence 6, Application US/07668648
XX
CC      SEQUENCE 6, Application US/07668648
CC      Patent No. 5416192
CC      GENERAL INFORMATION:
CC      APPLICANT: Shoyab, Mohammed
CC      APPLICANT: PLOWMAN, Gregory D.
CC      TITLE OF INVENTION: EPITHELIALS: NOVEL CYSTEINE-RICH GROWTH
CC      TITLE OF INVENTION: MODULATING PROTEINS
CC      NUMBER OF SEQUENCES: 12
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XX      SEQUENCE 6, Application US/08429998
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DE Sequence 6, Application US/08429998
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CC      Patent No. 5885961
CC      GENERAL INFORMATION:
CC      APPLICANT: Shoyab, Mohammed
CC      APPLICANT: PLOWMAN, Gregory D.
CC      TITLE OF INVENTION: EPITHELIALS: NOVEL CYSTEINE-RICH GROWTH
CC      TITLE OF INVENTION: MODULATING PROTEINS
CC      NUMBER OF SEQUENCES: 12
CC      CORRESPONDENCE ADDRESS:
CC      ADDRESS: Pennie & Edmonds
CC      STREET: 1155 Avenue of the Americas
CC      CITY: New York
CC      STATE: New York
CC      COUNTRY: USA
CC      ZIP: 10036
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Floppy disk
CC      COMPUTER: IBM PC compatible
CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      SOFTWARE: Patentin Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/08/429,998
CC      FILING DATE: 27-APR-1995
CC      CLASSIFICATION: 514
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: US 07/668,648
CC      FILING DATE: 13-MAR-1991
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: MISROCK, S. Leslie
CC      REGISTRATION NUMBER: 18,872
CC      REFERENCE/DOCKET NUMBER: 5624-161-999
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: (212)790-9090
CC      TELEFAX: (212) 869-9741
CC      INFORMATION FOR SEQ ID NO: 6:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 589 amino acids
CC      TYPE: amino acid
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: protein
SQ      SEQUENCE 589 AA; 63501 MW; 1690383 CN;

Query Match      37.6%; Score 53; DB 2; Length 589;
Best Local Similarity 35.7%; Pred. No. 6.38e+01;
Matches      5; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Db 560 HCSARGTKCLRKKI 573
QY 4 HOGTKSSKCVRKV 17
      | : : : : | : | :
      | : : : : | : | :

RESULT 13
ID US-07-668-648-6 STANDARD; PRT; 589 AA.
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AC xxxxxx
XX
DT
DE
DE Sequence 6, Application US/07668648
XX
CC      SEQUENCE 6, Application US/07668648
CC      Patent No. 5416192
CC      GENERAL INFORMATION:
CC      APPLICANT: Shoyab, Mohammed
CC      APPLICANT: PLOWMAN, Gregory D.
CC      TITLE OF INVENTION: EPITHELIALS: NOVEL CYSTEINE-RICH GROWTH
CC      TITLE OF INVENTION: MODULATING PROTEINS
CC      NUMBER OF SEQUENCES: 12
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CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Pennie & Edmonds
CC STREET: 1155 Avenue of the Americas
CC CITY: New York
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 10036
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/668,648
CC FILING DATE: 19910819
CC CLASSIFICATION: 514
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Mistrock, S. Leslie
CC REGISTRATION NUMBER: 18,872
CC REFERENCE/DOCKET NUMBER: 5624-161-999
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212)790-9090
CC TELEFAX: (212) 869-9741
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 589 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 589 AA; 63501 MW; 1690383 CN;
SQ
Query Match 37.6%; Score 53; DB 1; Length 589;
Best Local Similarity 35.7%; Pred. No. 6,386+01;
Matches 5; Conservative 7; Mismatches 2; Indels 0; Gaps 0;
Db 560 HCSARGTKLCRRKI 573
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4 HOGTKSSKCVROKV 17
QY
RESULT 14
ID PCT-US95-07754A-6 STANDARD; PRT; 652 AA.
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XX
XX
DE Sequence 6, Application PC/TUS9507754A
XX
CC Sequence 6, Application PC/TUS9507754A
CC GENERAL INFORMATION:
CC APPLICANT: Baker, Barbara J
CC APPLICANT: Whitlam, Steven A
CC TITLE OF INVENTION: Plant Virus Resistance Gene and Methods
CC NUMBER OF SEQUENCES: 6
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Margaret A. Connor, USDA-ARS
CC STREET: 800 Buchanan Street
CC CITY: Albany
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 94710
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/07754A
CC FILING DATE:
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Connor, Margaret A

CC REGISTRATION NUMBER: 30043
CC REFERENCE/DOCKET NUMBER: 0094.94
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (510) 559-6067
CC TELEFAX: (510) 559-5777
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 652 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 652 AA; 75261 MW; 2155152 CN;
SQ
Query Match 37.6%; Score 53; DB 4; Length 652;
Best Local Similarity 31.3%; Pred. No. 6,386+01;
Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
Db 156 DNRKTDADCIHQYD 171
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3 DHGTRSSKCVROKVE 18
QY
RESULT 15
ID US-08-261-663A-6 STANDARD; PRT; 652 AA.
XX xxxxxx
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XX
XX
XX
DE Sequence 6, Application US/08261663A
XX
CC Sequence 6, Application US/08261663A
CC Patent No. 5571706
CC GENERAL INFORMATION:
CC APPLICANT: Baker, Barbara J
CC APPLICANT: Whitlam, Steven A
CC TITLE OF INVENTION: Plant Virus Resistance Gene and Methods
CC NUMBER OF SEQUENCES: 6
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Margaret A. Connor, USDA-ARS
CC STREET: 800 Buchanan Street
CC CITY: Albany
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 94710
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/261,663A
CC FILING DATE:
CC CLASSIFICATION: 800
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Connor, Margaret A
CC REGISTRATION NUMBER: 30043
CC REFERENCE/DOCKET NUMBER: 0094.94
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (510) 559-6067
CC TELEFAX: (510) 559-5777
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 652 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 652 AA; 75261 MW; 2155152 CN;
SQ
Query Match 37.6%; Score 53; DB 1; Length 652;
Best Local Similarity 31.3%; Pred. No. 6,386+01;
Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Db 156 DNRKTDADCIRQIVD 171
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QY 3 DHQGTKSSKCVROKVE 18

Search completed: Wed Sep 6 08:17:55 2000
Job time : 9 secs.

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 12, 2000, 19:19:44 ; Search time 1890.83 Seconds

(without alignments)
705.070 Million cell updates/sec

Title: US-08-487-283A-8

Perfect score: 747
Sequence: 1 ARGCCGATATCCAGATGAC.....TGGTCACTGCTCGAGCTGA 747

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 972840 seqs, 892348106 residues

Total number of hits satisfying chosen parameters: 1945680

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBml:*
1: gb_bal:*
2: gb_bal2:*
3: gb_om:*
4: gb_ov:*
5: gb_pat:*
6: gb_ph:*
7: gb_pl1:*
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16: em_fun:*
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18: em_hum2:*
19: em_in:*
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62: em_htg4:*
63: em_htg5:*
64: em_htg6:*
65: em_htg7:*
66: em_hum6:*
67: gb_htg18:*
68: gb_htg19:*
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71: gb_htg22:*
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73: gb_htg24:*
74: gb_htg25:*
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77: gb_htg28:*
78: gb_htg29:*
79: gb_htg30:*
80: gb_htg31:*
81: gb_v11:*
82: gb_v12:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	294	39.4	819	5 A18692	A18692 Synthetic n
2	283.4	37.9	723	5 AR003797	AR003797 Sequence
3	283.4	37.9	723	5 AR010133	AR010133 Sequence
4	283.4	37.9	723	5 AR055339	AR055339 Sequence
5	283.4	37.9	723	5 I11980	I11980 Sequence 92
6	283.4	37.9	723	5 I40550	I40550 Sequence 89
7	262	35.1	888	14 AF132308	AF132308 Synthetic
8	258.6	34.6	902	14 XX049832	XX049832 Synthetic s
9	250	33.5	729	5 AR027053	AR027053 Sequence
10	250	33.5	729	5 I13036	I13036 Sequence 3
11	250	33.5	729	23 E10362	E10362 cDNA encodl
12	249.2	33.4	780	14 SYN198SCF	SYN198SCF
13	247.2	33.1	916	5 I45604	I45604 Sequence 29
14	245.6	32.9	828	12 MM295478	MM295478 Mus musculu
15	239.6	32.1	1149	5 A63778	A63778 Sequence 42
16	239.6	32.1	1212	5 A63772	A63772 Sequence 36
17	239.6	32.1	1422	5 A63768	A63768 Sequence 32
18	239.6	32.1	1545	5 A63770	A63770 Sequence 34
19	239.6	32.1	1956	5 A63776	A63776 Sequence 38
20	239.6	32.1	2079	5 A63776	A63776 Sequence 40
21	239.4	32.0	801	14 AF027160	AF027160 Synthetic
22	236.6	31.7	733	5 AR027763	AR027763 Sequence
23	234.4	31.4	721	5 AR027762	AR027762 Sequence
24	232.8	31.2	720	5 E13599	E13599 DNA encodin

Db 121 GGGAAACCTCCTAAGACCTGATCTATCGTCAACACATTTGGAAATCTGGGGTCCCATCA 180
QY 187 CGCTTCTGTGATCCGCTCCGGAACGGATTTCACTTACCATCAGCAAGTCTGAGAGCT 246
Db 181 AGGTTCAGTGGCAGTGGATCTGGGACAGATTAATCTCAGCATCAGACAGCTGCAATAT 240
QY 247 GAAGACTTTCCTGATGATTTACTGTCAAGACCTTTTAAATCTCCGTGACTTTGCGACAG 306
Db 241 GAAGATTTTGAATTTATTTATTTGTCACACAGATGATGAGTCTCCGTGACGTTGCGTGA 300
QY 307 GATACCAAGGAGGAAATTAACGTAAGTGGCGGTGGTGTCTGTGGGGGTTGAGATCTGCT 366
Db 301 GGACACCAAGCTTGAGATGAAA-----GGTGGCGGTGGATCTGTGGAGGTGGGTCGGA 354
QY 367 GGTGGCGGTCTCAAGTCCCAACTGATCGGATCCGCGCCGAGTCAAGAACCAAGGAGGCC 426
Db 355 GGTGGAGGATCTGAGATCTCAAGTGTGATGATCTGAGAGAGGCGCTGTAAGCTTGGAGG 414
QY 427 TCAGTCAAAAGTGTCTGTAAAGCTAGCGGCTATATTTTCTAATTTATTTGATTCATG 486
Db 415 TCCGTGAGATCTCTCGGACGCTTCTGGTATACCTTCACAAACTATGATGAACTGG 474
QY 487 GTGCGTCAAGGCCCCCGGAGGAGGCTGGAATGATGGGTGAGATCTTACCGGCTCTGCT 546
Db 475 GTGCGCAGGCTCCAGGAAAGGTTTAAAGTGAGTGGGCTGGATTAACACCCACACTGGA 534
QY 547 AGCACCAGATATACGAAATTTTAAAGACCGTGTACTATGACGCGTGAACCTCGACT 606
Db 535 GAGCCACATATGCTGATTTCTTCAAGGAGCGGTTTACCTTCTTGGAGCATCTAAG 594
QY 607 AGTACAGTATACATGAGAGCTCTCCAGCTGCGATCGAGAGACAGCGCGCTATATTATTC 666
Db 595 AACACTGCTATTTACAGATCAACAGCCTCAGAGCGGACGAGCGCTGTGATTTCTGT 654
QY 667 GCGCGTATTTTGTGTTCTAGCCCAATTTGATTTGATGTTTGGGGTCAAGGAAC 726
Db 655 ACAAGACGGGGTTACG-----ACTGTACTTCTGATGCTGGGGCCCAAGGAGAC 702
QY 727 CTGTCTACTGTCTCGAGCTGA 747
Db 703 ACGGTACCGTCTCTCATGA 723

RESULT 3
LOCUS AR010133 723 bp DNA PAT 04-DEC-1998
DEFINITION Sequence 89 from patent US 5756699.
ACCESSION AR010133
VERSION AR010133.1 GI:3968938
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 723)
AUTHORS Better,M.D., Carroll,S.F. and Studnicka,G.M.
TITLE Immunotoxins comprising ribosome-inactivating proteins
JOURNAL Patent: US 5756699-A 89 26-May-1998;
FEATURES
source 1..723
BASE COUNT 178 a 162 c 207 g 176 t
ORIGIN

Query Match 37.9%; Score 283.4; DB 5; Length 723;
Best Local Similarity 63.7%; Pred. No. 5.3e-71;
Matches 472; Conservative 0; Mismatches 251; Indels 18; Gaps 2;

QY 67 ATACCTGGCGGCCGACGCAAAACATCTATGGCGGCTAACTGGTATACGTAACT 126
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QY 127 GGGAAAGCTCCGAGCTTCTGATTTTACGTTGGAGGAACCTGCGAGATGAGATCCCTTCT 186
Db 121 GGGAAAGCTCCGAGACCTGATCTATGCTGCAACACAGTTGGAATCTGGGGTCCCATCA 180
QY 187 CGCTTCTGTGATCCGCTCCGGAACGGATTTCACTTACCATCAGCAAGTCTGAGAGCT 246
Db 181 AGGTTCAGTGGGAGTGGAGATCTGGGACAGATTAATCTCTACCATCAGACGCTGCAATAT 240
QY 247 GAAGACTTTCCTGATGATTTACTGTCAAGACGTTTAAATACTCCGTGACTTTGCGACAG 306
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QY 307 GGTACCAAGTGGAAATTAACGTAAGTGGCGGTGGTGTCTGTGGGGTGGAGATCTGCT 366
Db 301 GGACACCAAGCTTGAGATGAAA-----GGTGGCGGTGGATCTGTGGAGGTGGGTCGGA 354
QY 367 GGTGGCGGTCTCAAGTCCCAACTGATCGGATCCGCGCCGAGTCAAGAACCAAGGAGGCC 426
Db 355 GGTGGAGGATCTGAGATCTCAAGTGTGATGATCTGAGAGAGGCGCTGTAAGCTTGGAGG 414
QY 427 TCAGTCAAAAGTGTCTGTAAAGCTAGCGGCTATATTTTCTAATTTATTTGATTCATG 486
Db 415 TCCGTGAGATCTCTCGGACGCTTCTGGTATACCTTCACAAACTATGATGAACTGG 474
QY 487 GTGCGTCAAGGCCCCCGGAGGAGGCTGGAATGATGGGTGAGATCTTACCGGCTCTGCT 546
Db 475 GTGCGCAGGCTCCAGGAAAGGTTTAAAGTGAGTGGGCTGGATTAACACCCACACTGGA 534
QY 547 AGCACCAGATATACGAAATTTTAAAGACCGTGTACTATGACGCGTGAACCTCGACT 606
Db 535 GAGCCACATATGCTGATTTCTTCAAGGAGCGGTTTACCTTCTTGGAGCATCTAAG 594
QY 607 AGTACAGTATACATGAGAGCTCTCCAGCTGCGATCGAGAGACAGCGCGCTATATTATTC 666
Db 595 AACACTGCTATTTACAGATCAACAGCCTCAGAGCGGACGAGCGCTGTGATTTCTGT 654
QY 667 GCGCGTATTTTGTGTTCTAGCCCAATTTGATTTGATGTTTGGGGTCAAGGAAC 726
Db 655 ACAAGACGGGGTTACG-----ACTGTACTTCTGATGCTGGGGCCCAAGGAGAC 702
QY 727 CTGTCTACTGTCTCGAGCTGA 747
Db 703 ACGGTACCGTCTCTCATGA 723

RESULT 4
LOCUS AR055339 723 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 89 from patent US 5837491.
ACCESSION AR055339
VERSION AR055339.1 GI:5980916
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 723)
AUTHORS Better,M.D., Carroll,S.F. and Studnicka,G.M.
TITLE Polynucleotides encoding gelonin sequences
JOURNAL Patent: US 5837491-A 89 17-NOV-1998;
FEATURES
source 1..723
BASE COUNT 178 a 162 c 207 g 176 t
ORIGIN

Query Match 37.9%; Score 283.4; DB 5; Length 723;
Best Local Similarity 63.7%; Pred. No. 5.3e-71;
Matches 472; Conservative 0; Mismatches 251; Indels 18; Gaps 2;

ACCESSION AR027053
VERSION AR027053.1 GI:5937893
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 729)
Shimamura,T., Hamuro,J., Nakazawa,H., Kanayama,Y., Sugamura,K. and
Takeshita,T.
TITLE gamma-chain humaninterleukin-2 receptor polypeptide and method of
making
JOURNAL Patent: US 5856140-A 3 05-JAN-1999;
FEATURES Location/Qualifiers
source 1..729
BASE COUNT 199 a 169 c 182 g 179 t
ORIGIN
Query Match 33.5%; Score 250; DB 5; Length 729;
Best Local Similarity 60.9%; Pred. No. 2.3e-61;
Matches 447; Conservative 0; Mismatches 275; Indels 12; Gaps 2;
QY 7 GATATCCAGATGACCCGCTCCCTGCTCCGCTCTGTCGGCGATAGGGTCACC 66
DB 4 GATATTCCTGTCACACAGTCTCCAGCTCCCTATCTGCATCTGTGGAGAAACTGTACC 63
QY 67 ATACCTGGCGGCGCCAGCGAAACATCTATGGCCGCTGAACTGCTATCAACGTAACT 126
DB 64 ATACATGTGCGCAAGTGGGAATATTCACAAATTATTAGCATGTATCAGACAGAACAG 123
QY 127 GGGAAAGCTCGAAGCTTCTGATTTACGTGCGACGAACCTGGAGATGGATCCCTCT 186
DB 124 GGAATTCCTCCTACGCTCCGTGTATATGCAAAAACCTTAGCATGTGTGCTCATCA 183
QY 187 CGCTTCTTGATCCGGCTCCGGAACGATTTCACTGTGACCATCAGCATGTGACGCT 246
DB 184 AGGTTCAGTGGCAGTGGATCAGGAACACAAATATCTCTCAAGATCAACAGCTGAGCCT 243
QY 247 GAAGACTGCGCTACGTATTTACTGTCAGAAAGCTTTAAATCTCCGTGACTTTGGACAG 306
DB 244 GAAGATTTTGGAGATTATCTGTCAACATTTTGGAGTACTCCGTGACGCTTGGTGA 303
QY 307 GGTACCAAGTGGAAATAAACAATGACGTGGGGTGTGTGCTGGGGGGGTGATCTGGT 366
DB 304 GGGACCAAGCTGGAGCTCAAA-----GTGAGAAATCTCAGAGTCTGGCTCCGAA 354
QY 367 GGTGGGGTCTCAAGTCAACTGTGCAATCCGGCCGAGTCAAGAAAGCGGGGCC 426
DB 355 TCCAAAAGCAGCAGGTCAACTGAGAGATGTGACCTGAGCTGTGTGAACCTGGGGCT 414
QY 427 TCAGTCAAAAGTCTGTAAAGCTAGCGGCTAATATTTTCTAATATTATGATTCATAG 486
DB 415 TCAGTAAAGTATCTGCAAGGCTTGTGTACTCATCTGCTACTACATGACACTG 474
QY 487 GTCCGTCAGGCCCCCGGCGAGGGCTGGATGATGGGTGAGATCTTACCGGGCTCTGGT 546
DB 475 GTGAAACCAAGCCATGAAAGAGCTTGAGTGTGAGCTATTAATCCTTAACATGCT 534
QY 547 AGCAGCAATATACCGAAATTTTAAAGCGGTGTACTATGACGCGTACACTTCGACT 606
DB 535 GCTACTAGTACACCAAGAAATTTTCAAGGACAAAGCCAGCTTGATGTAGATTAAGTCTCC 594
QY 607 AGTACAGTATACATGAGCTCTCCAGCTCGATCGAGAGACAGCGCGCTATTATTC 666
DB 595 AGCAGCCTACATGAGCTCCACAGCTCAGACATCTGAGAGCTCTGAGCTATTACTGT 654
QY 667 GCGCGTATTTTGGTCTAGCCCAATGTGATTTGATGTTGGGTCAAGGAAC 726
DB 655 GCAAGAGAGATTTACTACGGTAGTAGCTACGGG---TTTGGTACTGGGCGCAAGGGACT 711
QY 727 CTGTGACTGTCTC 740
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DB 712 CTGTGACTGTCTC 725
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LOCUS I31036 729 bp DNA PAT 06-FEB-1997
DEFINITION Sequence 3 from patent US 5582826.
ACCESSION I31036
VERSION I31036.1 GI:1821827
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 729)
Shimamura,T., Hamuro,J., Nakazawa,H., Kanayama,Y., Sugamura,K. and
Takeshita,T.
TITLE Monoclonal antibodies which bind the gamma chain of human
interleukin-2 receptor
JOURNAL Patent: US 5582826-A 3 10-DEC-1996;
FEATURES Location/Qualifiers
source 1..729
BASE COUNT 199 a 169 c 182 g 179 t
ORIGIN
Query Match 33.5%; Score 250; DB 5; Length 729;
Best Local Similarity 60.9%; Pred. No. 2.3e-61;
Matches 447; Conservative 0; Mismatches 275; Indels 12; Gaps 2;
QY 7 GATATCCAGATGACCCGCTCCCTGCTCCGCTCTGTCGGCGATAGGGTCACC 66
DB 4 GATATTCCTGTCACACAGTCTCCAGCTCCCTATCTGCATCTGTGGAGAAACTGTACC 63
QY 67 ATACCTGGCGGCGCCAGCGAAACATCTATGGCCGCTGAACTGCTATCAACGTAACT 126
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DB 355 TCCAAAAGCAGCAGGTCAACTGAGAGATGTGACCTGAGCTGTGTGAACCTGGGGCT 414
QY 427 TCAGTCAAAAGTCTGTAAAGCTAGCGGCTAATATTTTCTAATATTATGATTCATAG 486
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QY 487 GTCCGTCAGGCCCCCGGCGAGGGCTGGAAATGATGGGTGAGATCTTACCGGGCTCTGGT 546
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RESULT 11
E10362 ID E10362 standard; RNA; ROD; 729 BP.
AC E10362;
XX E10362.1
SV
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XX 08-OCT-1997 (Rel. 52, Created)
DT 08-OCT-1997 (Rel. 52, Last updated, Version 1)
XX
XX cDNA encoding an monoclonal antibody against human Interleukin-2
DE receptor gamma chain.
DE
XX JP 1995313188-A/2.
XX
XX Mus sp.
OS
OC Eukaryota; Metazoa; Chordata; Vertebrata; Teleostomi;
OC Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
OC Mus.
XX [1]
XX 1-729
RA Shimamura T., Hamuro J., Nakazawa H., Kanayama Y., Sugamura K.,
RA Takeshita T.;
RT "TMUNOSUPPRESSIVE AGENT";
RL Patent number JP 1995313188-A/2, 05-DEC-1995.
RL AJINOMOTO CO INC, SUGAMURA KAZUO..
XX
XX Mus sp. (mouse)
CC
CC PN JP 1995313188-A/2
CC PD 05-DEC-1995
CC PF 21-APR-1994 JP 1994082836
CC PR 21-APR-1993 JP 93P 94491, 07-MAR-1994 JP 94P 36065
CC PI SHIMAMURA TOSHIAKI, HAMURO JUNJI, NAKAZAWA HARUMI,
CC PI KANAYAMA YUKA,
CC PI SUGAMURA KAZUO, TAKESHITA TOSHIICHI
CC PC C12P21/08.A61K39/395.A61K39/395.C12N1/21.C12N5/20,
CC PC C12N15/13//C12N15/06,
CC PC (C12P21/08.C12R1:19).(C12P21/08.C12R1:91).(C12N1/21.C12R1:19);
CC FH Key Location/Qualifiers
CC FT source 1..729
CC FT /organism="Mus sp."
CC FT /cell_type="hybridoma"
CC FT /cell_line="GP-4"
CC FT mat_peptide 1..729
CC FT /product="anti-IL-2 receptor gamma chain"
CC FT Location/Qualifiers
XX
XX source 1..729
XX /db_xref="taxon:10095"
XX /organism="Mus sp."
XX
XX Sequence 729 BP; 199 A; 169 C; 182 G; 179 T; 0 other;

Query Match 33.5%; Score 250; DB 23; Length 729;
Best Local Similarity 60.9%; Pred. NO. 2.3e-61;
Matches 447; Conservative 0; Mismatches 275; Indels 12; Gaps 2;

QY 7 GATATCCAGATGACCCAGTCCCGCTCCCTGCTCCGCTCTGTGGCGATAGGGTCACC 66

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Db 4 GATATTCGTGACACAGTCTCCAGCTCCCTATCGCATCTGTGGGAGAAACTGTCCACC 63
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QY 67 ATCACTCGGGCCAGCGAAACATCTATGCGCGCTCAACTGGTATCAAGTAAACCT 126
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QY 127 GGGAAAGCTCCGAAGCTTCTGATTTTACGGTGGGAGCAACCTGGCAGATGGAGTCCCTTCT 186
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QY 187 CGCTTCTCTGGATCCGGTCCGGAACGGATTTCACTCTGACCATCAGCAGTCTGACGCT 246
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QY 727 CTGCTCACTGCTC 740
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Db 712 CTGCTCACTGCTC 725
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RESULT 12
SYNN198SCF
LOCUS SYNN198SCF 780 bp DNA SYN 22-JUN-1995
DEFINITION Synthetic single chain Fv (N19-8 scFv) DNA fragment.
ACCESSION L43067
VERSION L43067.1 GI:870721
KEYWORDS complement C5 inhibitor; inclusion body protein.
SOURCE Synthetic construct DNA.
ORGANISM Synthetic construct
          artificial sequence.
REFERENCE 1 (bases 1 to 780)
AUTHORS Evans, M.J., Rollins, S.A., Wolff, D.A., Rother, R.P., Norin, A.J.,
          Th.D.M., Mueller, J.P., Nye, S.H., Squinto, S.P., and Wilkins, J.A.
TITLE In vitro and in vivo inhibition of complement activity by a
          single-chain Fv fragment recognizing human C5
JOURNAL Mol. Immunol. (1995) in press
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Db	61	GCCACCATATCTCTGAGAGACCCAGTGAAAGTGTGATAGTATGACAAATAGTTTATGCAC	120	
OY	109	TGGTATCAACGTMAACTTGGGAAGCTCCGAGCTTCGTGATTTACGGTGCAGAACCTG	168	
Db	121	TGGTACGACAGAAACAGAGACAGCCACCACCAATCTCATCTTTCTTGCATCCACCTA	180	
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Db	181	GAATCTGGGGTCCCTCCAGGTTCAATGAGCAGTGGGATGAGACAGACTTCACCTCAC	240	
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Db	241	ATTGATCTGTGGAGGCTGTATGATCTCTCAACCTTATCTGTACACAAATATAGAGTT	300	
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Db	301	CCGAACAGCTTCGGAGGGGGAGCAAGCTGGAAATTAACGGACCGAGGTGGCGTGC	360	
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Db	361	GGTGGCGGGGATCGGGGTGGCGAGGGTTCGACGTCACAGCTGTGTGAGTCTGGGGAGAC	420	
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DEFINITION Sequence 29 from patent US 5637481.
ACCESSION  I45604
VERSION     I45604.1  GI:2469706
KEYWORDS
SOURCE      Unknown:
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 916)
AUTHORS     Ledbetter,J.A., Gilliland,L.K., Hayden,M.S., Linsley,P.S.,
            Bajorath,J. and Fell,H.Perry.
TITLE       Expression vectors encoding bispecific fusion proteins and methods
            of producing biologically active bispecific fusion proteins in a
            mammalian cell
JOURNAL     Patent: US 5637481-A 29 10-JUN-1997;
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Matches 449; Conservative 0; Mismatches 288; Indels 9; Gaps 2

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Query Match	33.1%	Score 247.2	DB 5	Length 916
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QY	535	CGGGCTCTGGTAGACCGCAATATACCGAAATTTTAAAGACCGTGTACTATGACGGAT	594	
Db	613	CCATACAAAGGCTTACTACTCTACACACCGAATTTTAAAGGGCAGAGCCACCATTAATCTGA	672	
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Job time: 4618 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 12, 2000, 19:06:43 ; Search time 930.19 Seconds
(without alignments)
3541.364 Million cell updates/sec

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Perfect score: 747
Sequence: 1 ATGCCGATATCCAGATGAC.....TGGTCACTGTCTCGAGCTGA 747

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5247842 seqs, 2204914090 residues 10495684
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
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Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	189.4	25.4	493	72	AW405753 UI-HF-BL0
3	186.2	24.9	487	72	AW405301 UI-HF-BL0
4	184.6	24.7	471	72	AW406294 UI-HF-BL0
5	184.6	24.7	566	72	AW406081 UI-HF-BL0
6	183.2	24.5	608	72	AW404714 UI-HF-BL0
7	183	24.5	431	72	AW406886 UI-HF-BL0
8	183	24.5	447	72	AW405752 UI-HF-BL0
9	182.8	24.5	460	72	AW405906 UI-HF-BL0
10	182.8	24.5	653	71	AW391263 QVO-ST021
11	179.8	24.1	391	72	AW404992 UI-HF-BL0
12	179.8	24.1	453	71	AW383563 PM4-HT034
13	179.4	24.0	488	72	AW403591 UI-HF-BL0
14	176.6	23.6	426	72	AW405900 UI-HF-BL0
15	176.6	23.6	466	72	AW406828 UI-HF-BL0
16	175.2	23.5	413	24	AA301347 EST14279
17	175	23.4	418	72	AW404507 UI-HF-BL0
18	172.4	23.1	460	72	AW406939 UI-HF-BL0
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22	171.8	23.0	496	72	AW404748 UI-HF-BL0
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26	167.8	22.5	508	72	AW403684 UI-HF-BL0
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DEFINITION IMAGE:3061128 5', mRNA sequence. 16-FEB-2000 EST

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AW407904
AW407904.1 GI:6926961
EST.
human.
Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 422)
NIH-MGC <http://www.ncbi.nlm.nih.gov/MGC/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
On Jan 6, 2000 this sequence version replaced gi:6676952.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
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M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonafide, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT
ORIGIN

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Query Match
Best Local Similarity
Matches 250; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

26.0%; Score 194.2; DB 72; Length 422;

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DB 143

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QY 187

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DB 203

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QY 247

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DB 263

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DB 323

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[illegible]

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ORGANISM	Homo sapiens		
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AUTHORS	1 (bases 1 to 487)		
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JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	On Jul 8, 1999 this sequence version replaced gi:5421949.		
	Contact: Robert Strausberg, Ph.D.		
	Tel: (301) 496-1550		
	Email: Robert.Strausberg@nih.gov		
	Eco RI site shown at the beginning of the sequence.		
	Tissue Procurement: Louis M. Staudt, M.D., Ph.D.		
	cDNA Library Preparation: M.B. Soares Lab		
	cDNA Sequencing by: M.B. Soares Lab		
	DNA distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/BLN at:		
	www.bio.lnl.gov/db/ftp/Image/Image.html		
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	M. Staudt, Ph.D. Library preparation by Maria de Fatima		
	Bonafide, Ph.D. and M. Bento Soares, Ph.D."		
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7	GATATCCAGATGACCCAGTCCCGCTCCCTCCGTCCGCGCTGTGGCGCATAGGTCACC	66	
Db			
42	GACATCCAGATGATGACCAAGTCCGATCTCCCTGTGCACTGTGAGAGACAGAGTACAC	101	
67	ATCACCCTGGGGCGCCAGCGAAGACATCTATGGCGCGCTGAACCTGGTATTAACGTAACT	126	
Db			
102	ATCACTTCCCGGGCAGTCAGAGCATTTAGACACTATTTTAAATTGGTATCAGCAAGAACCA	161	
127	GGGAAGTCCGGAACCTTCTGATTTACGGTGGGAGGAACCTGGCAGATGGAGTCCCTTCT	186	
Db			
162	GGGAAGCCCTTAATCTCTGATTTATGTGTCATCATTTTGGCAAGTGGGTCCTATCA	221	
187	CGCTTCTCTGATCCGGCTCCGGAACGATTTCACTCTGACCATCAGCATCTGCAGCCT	246	
Db			
222	AGGTCAATGGGAGTGTGGAGACAGATTTCACTCTACCATCAGCATGTGTGCAACT	281	
247	GAGACCTTCGCTAGCTATTACTGTGCAGAACGTTTAAATATCTCCGTTGACTTTCGACAG	306	

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Db 282 GAAGATTTGCAACTTACTACTGTCAACAGAGTTACAGTGGCCCGTACAGTTTGGCCAG 341
QY 307 GGTACCAAGTGGAAATAAAAGTACTGGCGTGTGGTGTCTTG 349
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Db 342 GGGACCAAGCTAGATCAACAGCACTGTGGTGCACCATCTG 384

RESULT 4
LOCUS AW406294 471 bp mRNA EST 16-FEB-2000
DEFINITION UI-HF-BLO-aco-b-09-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3059657 5', mRNA sequence.
ACCESSION AW406294
VERSION AW406294.1 GI:6925351
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 471)
AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On May 11, 1999 this sequence version replaced gi:4776604.
Contact: Robert Strausberg, Ph.D.
Email: Robert.Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbp/image/image.html
Seq primer: M13 Forward.
FEATURES
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                /note="Vector: p7T3-Pac; Site_1: NotI; Site_2: Eco RI;
                Constructed from size fractionated cytoplasmic mRNA
                (1.5-2.5kb). Directionally cloned. Cells provided by Louis
                M. Staudt, Ph.D. Library preparation by Maria de Fatima
                Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 115 a 132 c 110 g 114 t

Query Match 24.7%; Score 184.6; DB 72; Length 471;
Best Local Similarity 71.1%; Pred. No. 1.7e-46;
Matches 244; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 7 GATATCCAGATGACCCAGTCCCGCTCCCTCCCTGTCGGCTGTGGCGATAGGGTCACC 66
Db 57 GACATCCAAATGACCCAGTCTCCATCCCTGTCGTCATCTGTAGGAGACAGAGTCACC 116

QY 67 ATCACTCGGGCCAGGAAACATCTATGGCGCGCTGAACCTGGTATCAAGCTAAACCT 126
Db 117 ATCACTTCGGACAAAGTCACAGCATTAGAACCTATTTAAATGGTATCAGCAGAAACCA 176

QY 127 GGGAAAGCTCCGAAGCTTCTGATTACGGTGGCAGCAACCTGGCAGATGAGTCCCTTCT 186
Db 177 GGGAAAGCCCTTAACCTCTGATCTATGCTGATCAGCTTTCGAAGTGGGGTCCCATCA 236

QY 187 GCGTCTCTGATCGCGTCCCGAAGCGGATTTCACTCTGACCATCAGCAGTCTGCAGCCT 246
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Db 237 AGGTTCAAGTGGCAGTGGAFTCTGGACAGAGTTTCACTCTCACCATCAGCAGTCTGCAACCT 296
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Db 297 GAAGATTTTGGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGTGGAGCTTCGGCCCA 356
QY 307 GGTACCAAGTGGAAATAAAAGTACTGGCGTGTGGTGTCTTG 349
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Db 357 GGGACCAAGTGGAAAGTCAACGAACTGTGGTGCACCATCTG 399

RESULT 5
AW406081 566 bp mRNA EST 16-FEB-2000
LOCUS UI-HF-BLO-acy-b-03-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
DEFINITION IMAGE:3060700 5', mRNA sequence.
ACCESSION AW406081
VERSION AW406081.1 GI:6925102
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 566)
AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On May 11, 1999 this sequence version replaced gi:4776388.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbp/image/image.html
Seq primer: M13 Forward.
FEATURES
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                /cell_line="MGC85"
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                /note="Vector: p7T3-Pac; Site_1: NotI; Site_2: Eco RI;
                Constructed from size fractionated cytoplasmic mRNA
                (1.5-2.5kb). Directionally cloned. Cells provided by Louis
                M. Staudt, Ph.D. Library preparation by Maria de Fatima
                Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 138 a 157 c 143 g 128 t
ORIGIN

Query Match 24.7%; Score 184.6; DB 72; Length 566;
Best Local Similarity 71.1%; Pred. No. 1.8e-46;
Matches 244; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 7 GATATCCAGATGACCCAGTCCCGCTCCCTCCCTGTCGGCTGTGGCGATAGGGTCACC 66
Db 65 GACATCCAGATGACCCAGTCTCCATCCCTGTCGTCATCTGTAGGAGACAGAGTCACC 124

QY 67 ATCACTCGGGCCAGGAAACATCTATGGCGCGCTGAACCTGGTATCAAGCTAAACCT 126
Db 125 ATCACTTCGGGCAAGTCAGACATTAGCAGTTATATAAATGGTATCAGCAGAAACCA 184

QY 127 GGGAAAGCTCCGAAGCTTCTGATTACGGTGGCAGCAACCTGGCAGATGAGTCCCTTCT 186
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Db	105	ACTGCGGGGGAAGTCAGACGATTTAGCAGCTTTTAAATTGGTAATCCAGCAAAAATCAGGG	164
Oy	130	AAAGCTCCGAAGCTTCTGTATTTACGCTGCAGAACCTGGCAGATGAGATCCCTTCTGCC	189
Db	165	AAAGCCCCATACTCTGTATCTATCTGATCATCCATTTTGCAAATGGGGTCCCATCAAGG	224
Oy	190	TTCCTGTGATCCGGCTCCGGAAACGATTTCACTGTGACCATAGACAGTGTAGAGCTGAA	249
Db	225	TTCACTGGCAGTGTAGATCGGACAGATTTCACTGTCCATCAGCAGTGTGACACTGAA	284
Oy	250	GACTTCGCTACCTATTTACTGTGAGAAGCTTTTTAAATATCTCCGTTGACTTTCGACAGGT	309
Db	285	GATTTTGCACACTATTCTGTGTGACAGAGATTTCTACTACCCCGTAGAGTTTGGCCAGGG	344
Oy	310	ACCAGGTGGAAATAAACAAGTACTGGCGGTGGTGTCTG	349
Db	345	ACCAGACTGGAGATCAACGAACACTGTGGCTGCACCATCTG	384
RESULT	7		
LOCUS	AW406886	431 bp mRNA EST	16-FEB-2000
DEFINITION	UI-HF-BL0-aqg-h-06-0-UI.r1 NIH.MGC_37 Homo sapiens cDNA clone IMAGE:3061499 5', mRNA sequence.		
ACCESSION	AW406886		
VERSION	AW406886.1	GI:6925943	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria (to 431)		
AUTHORS	NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)		
COMMENT	On Jan 6, 2000 this sequence version replaced gi:6675906. Contact: Robert Strausberg, Ph.D. Tel.: (301) 496-1550 Email: Robert.Strausberg@nih.gov Eco RI site shown at the beginning of the sequence. Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: M.B. Soares Lab CDNA Library Arrayed by: M.B. Soares Lab DNA Sequencing by: M.B. Soares Lab Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: www.bio.lnl.gov/dbrr/image/image.html Seq primer: M13 Forward		
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	/clone_1lb="NIH_MGC_37"		
	/tissue_type="lymph"		
	/cell_type="germinal center B cells"		
	/cell_line="MGC85"		
	/lab_host="DH10B (LT)"		
	/note="Vector: pMT3-Pac; Site_1: NotI; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."		
BASE COUNT	101 a 125 c 105 g 100 t		
ORIGIN			
Query Match	24.5%	Score 183;	DB 72; Length 431;
Best Local Similarity	70.8%;	Pred. No. 5.2e-46;	
Matches 243;	Conservative	0; Mismatches 100;	Indels 0; Gaps 0;
7	CATATCCAGATGACCAAGTCCCCTGCTCCCTGTCGCCCTCTGTGGCGATAGGCTCAC	66	

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Db 60 GACATCCAGATGACCCAGTCTCCATCTCCCTGTCTGTCATCTGTAGGAGACAGATCACC 119
QY 67 ATCACTGCGCGCAGCGAGAAACATCATATGCGCGCTGAACCTGTATCAACGTAAACCT 126
Db 120 ATCACTTGGCGGCAAGTCAGAGCATATAGCAGCTTTTAAATTTGATGATCAGCAGAAACCA 179
QY 127 GGGAAAGCTCCGAAGCTTCTGATTACGCGTGCGAGCAACCTGGCAGATGGAGTCCCTTCT 186
Db 180 GGGAAAGCCCTCAGCTCCTGATCTATGGAGCATCCAGTTTCAAAAGTGGGTCCCATCA 239
QY 187 GCGTCTCTGATCCGCTCCGGAACGATTTCACTCTGACCATCAGCAGTCTGAGCCT 246
Db 240 AGGTTCAAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 299
QY 247 GAAGACTTCGCTAGCTATTACTGTGTCAGAACGTTTAAATATACCTGCTGACTTTTCGGACAG 306
Db 300 GAAGATTTGCAACTTACTACTGTCAACAGAGTTACACTACCCCTCGCAGCTTTTCGGGGA 359
QY 307 GGTACCAAGTGGAAATAAAACGTTACTGCGCGTGGTGGTCTG 349
Db 360 GGGACCAAGTGGAGATCAACGAACCTGTGGCTGCACCATCTG 402

RESULT 8
AW405752 447 bp mRNA EST 16-FEB-2000
LOCUS UI-HF-BLO-abp-a-01-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
DEFINITION IMAGE:3057288 5', mRNA sequence.
ACCESSION AW405752
VERSION AW405752.1 GI:6924809
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 447)
AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Aug 21, 1998 this sequence version replaced gi:3707751.
Contact: Robert Strausberg, Ph.D.
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M3 Forward.
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/lab_host="DH10B (LT1)"
/notes="Vector: pT73-Pac; Site1: NotI; Site2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 105 a 129 c 111 g 102 t
ORIGIN
Query Match 24.5%; Score 183; DB 72; Length 447;
Best Local Similarity 70.8%; Pred. No. 5.3e-46;

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Matches 243; Conservative 0; Mismatches 100; Indels 0; Gaps 0;
QY 7 GATATCCAGATGACCCAGTCCCGTCTCCCTGTCGCGCTCTGTGGCGATAGGTCACC 66
Db 83 GACATCCAGATGACCCAGTCTCCATCTCCCTGTGTCATCTGTAGGAGACAGTACC 142
QY 67 ATCACTTGGCGGCGCCAGCGAAACATCTATGGCGCTGAACCTGGTATCAACGTAAACCT 136
Db 143 ATCACTTGGCGGCGCAAGTCAGAGCATATAGCAGCTATTTAAATTTGATCAGCAGACCA 202
QY 127 GGGAAAGCTCCGAGAGCTTCTGATTACGCGTGCGACCAACCTGGCAGATGGAGTCCCTTCT 186
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QY 187 CGCTTCTCTGGATCCGCTCCGGAACGATTTTCACTCTGACCATCAGCAGTCTGACGCT 246
Db 263 ACCTTCAAGTGGCAGTGGATCTGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 322
QY 247 GAAGACTTCGCTACGTATTACTGTCAAGAGCTTTTAAATATCTCCGTTGACTTTTCGGACAG 306
Db 323 GAAGATTTTGCACACTTACTACTGTCAACAGAGCTACAGTACCCCGTACAGTCTTTTGGCCAG 382
QY 307 GGTACCAAGTGGAAATAAAACGTTACTGCGCGTGGTGGTCTG 349
Db 383 GGGACCAAGTGGAGATCAACGAACCTGTGGCTGCACCATCTG 425

RESULT 9
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LOCUS UI-HF-BLO-acg-a-12-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
DEFINITION IMAGE:3058847 5', mRNA sequence.
ACCESSION AW405906
VERSION AW405906.1 GI:6924963
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 460)
AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jul 8, 1999 this sequence version replaced gi:5422554.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
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/lab_host="DH10B (LT1)"
/notes="Vector: pT73-Pac; Site1: NotI; Site2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5Kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 107 a 128 c 113 g 112 t
ORIGIN

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[illegible]


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BASE COUNT      111 a      136 c      140 g      101 t
ORIGIN
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Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

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Query Match	24.08:	Score 179.4:	DB 72:	Length 488:
Best Local Similarity	67.68:	Pred. No. 7.1e-45:		
Matches 252:	Conservative 0:	Mismatches 121:	Indels 0:	Gaps
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Db	48	GTGGCCCACTCCCAAGTCAGGCTTGTGCAGTCTGGGGCTGAGGTGAAGAGGCTGGGGCTT	1070	
QY	428	CAGTCAAGTCTCTGTAAACCTAGCGGCTATTTTTTCTAATATTGGATTCAATGGG	4878	
Db	108	CAGTGAAGTTCCTGTGCAGGCTTCTGGAATACACTTCACCTAATAGCTAATATTGGG	1678	
QY	488	TGCGTCAGGCCCCCGGGCAGGGCTGGATGGATGGGTGAGATCTTACCGGGCTCTGGTA	5478	
Db	168	TGGCGCAGGGCCCCGGACAAGGCTTGAATGGATGGGATGGATGAAGGCTGGCAATAGTA	2277	
QY	548	GCACCGAATATACCGAAATTTTAAAGACGCTGTTACTATGACGCGTGACACTTGCAGTA	6078	
Db	228	ACACAAATATTTCCACAGAAAGTTTACGGCACAGCTCACCATTTGCCAGGGACACATCCCGCA	2878	
QY	608	GTACAGTATACATGAGCTCCACAGCTCGCATGGAGTGGAGACAGCGGCTCATATTGGG	6678	
Db	288	GCAACAGCTACATGTGAGCTGACGACGCTTGAGATTTGAAGACACGCGCTGTGATTACTGTG	3478	
QY	668	CGCGTATTTTTTGGTTCTAGCCCGCAATGGTATTTTGAATGTTGGGCTCAAGAACCC	7277	
Db	348	CGAAGCGGAGAAATTACTATGTTTCAGGAGATCTCTTGACTACTAGGGGCCAGGAACC	4078	
QY	728	TGTCATCTGTCTC	740	
Db	408	TGGTACCGTCTC	420	

RESULT 14					
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DEFINITION	U1-HF-BLO-acg-a-03-0-01.t1 NH_MGC_37 Homo sapiens cDNA clone IMAGE:3058829 5', mRNA sequence.				
ACCESSION	AM405900				
VERSION	AM405900.1	GI:6924957			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 426)				
TITLE	NH-MGC http://www.ncbi.nlm.nih.gov/MGC/ .				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)				
COMMENT	On May 11, 1999 this sequence version replaced gi:4776201.				

Email: Robert_Strausberg@nih.gov
 GEO R1 site shown at the beginning of the sequence
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: M.B. Soares Lab
 cDNA Library Arrayed by: M.B. Soares Lab

FEATURES
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1. 426
Location/Qualifiers
Seq primer: M13 forward.
www-bio.llnl.gov/bdip/image/image.html
found through the I.M.A.G.E. Consortium/LLNL at:
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be

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/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Banto Soares, Ph.D."

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	Query Match	23.68;	Score 176.6;	DB 72;	Length 426;
	Best Local Similarity	69.78;	Pred. No. 5e-74;		
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Db	11 GACATCCGATGACCCAGTCCATCTCCCTCGTCTGCATCTGTAGAGAGACAGTGTCACC	70			
QY	67 ATCACTCGGGCGGCCACCGAATAATCTATGCGCGCTGAACCTGGTATCAAGCTAAACT	126			
Db	71 ATCACTTCGCGGGGAGTCAGACGATTAGCAAGTATTTAAATGGTATCAAGCAAAAACA	130			
QY	127 GGGAAGAAGTCGAGAGCTTGTATTACGGTCCGAGAACCTGGCAGATGGAGTCCCTTCT	186			
Db	131 GGGAAAGCCCTTAAGCTCTGATCTCATCCAGATGATCCAAATTTGGAAACAGGGGTCCATCA	190			
QY	187 CGCTTCTCTGGATCCGGGCTCCGGAAGGATTTCACTGTGACCATCAGACGTCGACGCT	246			
Db	191 AGGTTCAAGTAGAATGGATCTGGACAGATTTTACTTTCACCAATCACGACGCTCAAGCT	250			
QY	247 GAAGACTTCGTTAGCTATTTACTGTGCAGAACGTTTTAAATACCTCCGTGACTTTGGACAG	306			
Db	251 GAAGATATTGGAAATATTTACTGTCAACAGATGATGATGCTCCCCCTTATTTGGCGGA	310			
QY	307 GGTCAACAAGGTGAAATAAACGTCATGGCGGCTGGTGGTCTG 349				
Db	311 GGGACCAAGGTGGAGATCAAACGAACTGTGGCTGCACCACATCTG 353				

RESULT	15
LOCUS	AM406828
DEFINITION	AM406828 466 bp mRNA EST 15-FEB-2000 UT-HF-BLO-aag-a-09-0-UI.r1 NR_HMGCC_37 Homo sapiens CDNA clone IMAGE:3061169 5' , mRNA sequence.
ACCESSION	AM406828
VERSION	AM406828.1 GI:6925885
KEYWORDS	EST .
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 466) NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/ . National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
TITLE	On Jan 6, 2000 this sequence version replaced gi:6675848.
JOURNAL	
COMMENT	

Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov

```

ECO RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
Location/Qualifiers
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/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/notes="Vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb) Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
109 a 125 c 116 g 116 t
BASE COUNT

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Search completed: September 12, 2000, 20:04:48
Job time: 3485 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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Run on:      September 12, 2000, 20:01:31
              (without alignments)
              2533.462 Million cell updates/sec
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Title: US-08-487-283A-8
Page: 747

Sequence: 1 ATGCCGATATCCAGATGAC.....TGGTCACTGTCTCGAGCTGA 747

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 311585 segs, 125096042 residues

Total number of hits satisfying chosen parameters: 623170

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

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Database : N_Geneseq_36: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	747	100.0	747	1	T08480	Humanised CDR-gra4d
2	729.4	97.6	747	1	T08488	Humanised CDR-gra4d
3	396.6	53.1	747	1	T08449	Murine 5G1.1M1 SCH
4	371	49.7	750	1	T08484	Humanised 5G1.1 VH
5	358.2	48.0	750	1	T08487	Humanised 5G1.1 VH
6	350.2	46.9	750	1	T08483	Humanised 5G1.1 VH
7	328.8	44.0	726	1	T110706	Humanised 5G1.1 VH
8	323.8	43.3	711	1	T08486	Humanised 5G1.1 VH
9	322.4	43.2	726	1	T08485	Humanised 5G1.1 VH
10	294	39.4	819	1	Q20381	Sequence encoding
11	283.4	37.9	723	1	Q42284	v-J(kappa)/(GLY)
12	267	35.7	1065	1	T94963	R. piplens recomb
13	267	35.7	1065	1	T94967	R. piplens recomb
14	267	35.7	1074	1	T94965	R. piplens recomb
15	267	35.7	1074	1	T94968	R. piplens recomb
16	267	35.7	1086	1	T94966	R. piplens recomb
17	267	35.7	1137	1	T94964	R. piplens recomb
18	250	33.5	729	1	Q73679	Fv(G γ 4) immunosu
19	249.2	33.4	783	1	T08490	Anti-C5 Mab N19/8
20	247.2	33.1	913	1	Q81076	Bispecific CD3-T6F8
21	239.6	32.1	1149	1	T90514	DNA encoding chime
22	239.6	32.1	1212	1	T90511	DNA encoding chime
23	239.6	32.1	1422	1	T90509	DNA encoding chime
24	239.6	32.1	1545	1	T90510	DNA encoding chime
25	239.6	32.1	1956	1	T90512	DNA encoding chime
26	239.6	32.1	1079	1	T90513	DNA encoding chime
27	236.6	31.7	733	1	T95976	A33/218 single-ch
28	236.6	31.7	1938	1	V58929	A33/218 single-ch
29	234.4	31.4	721	1	V99765	A33/212 single-ch
30	232.8	31.2	720	1	T91615	CDNA encoding an
31	232.4	31.1	2178	1	Q25592	Encodes 4D5 Fab I
32	232.4	31.1	2178	1	V81689	4D5 Fab molecule
33	231.6	31.0	5227	1	T79537	plasmid pRERMsc2H

45	231.8	30.9	6727	1	V63616
34	230.6	30.9	1299	1	V63620
35	230.6	30.9	1330	1	V63617
36	230.6	30.9	6799	1	V63619
37	230.6	30.5	2133	1	X03840
38	227.6	30.4	735	1	T91614
39	227	30.1	819	1	T35691
40	224.8	30.1	819	1	T86646
41	224.8	30.1	732	1	Q73678
42	224.4	30.0	732	1	Q73678
43	223.2	29.9	6127	1	X07474
44	221.6	29.7	720	1	Q55181
45	221.8	29.7	720	1	T65007

ALIGNMENTS

Query Match	100.0%	Score 747:	DB 1:	Length 747:
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1	ATGGCGGATATCCAGATGACCGCAGTCCCGCTCCCTGCTCCGCTCTGTGGCGGATAGG	60		
DB	1	ATGGCGGATATCCAGATGACCGCAGTCCCGCTCCCTGCTCCGCTCTGTGGCGGATAGG	60	
QY	61	GTACACATCACTCTGGGGGGCCGACGCAAAACATCTATGGCGCGCTGACATGGATCAAGT	120	
DB	61	GTACACATCACTCTGGGGGGCCGACGCAAAACATCTATGGCGCGCTGACATGGATCAAGT	120	
QY	121	AAACCTGGGAAAGCTCCGCAAGCTTGATTTACGGGCGCAGCAAGCTGGCAGATGGAGTC	180	
DB	121	AAACCTGGGAAAGCTCCGCAAGCTTGATTTACGGGCGCAGCAAGCTGGCAGATGGAGTC	180	
QY	181	CCCTTCGCTTCTCTGGATCCGGCTCCGGACGAGATTTCACCTGTACCTACGACAGTCTG	240	

OS	Mus sp.	location/qualifiers
FH	Key	1..747
FT	cds	/*tag= a
FN	W09529697-A1.	
FT	09-NOV-1995.	
PD	01-MAY-1995.	
PR	02-MAY-1994; US-236208.	
PA	(ALEX-) ALEXION PHARM INC.	
PI	Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S;	
PI	Rother RP, Springhorn J P, Squanto SP, Thomas TC;	
PI	Wang Y, Wilkins JA;	
DR	WPI: 95-382923/50.	
DR	P-PSDB: R77606.	
PT	Treating glomerulonephritis with antibody against complement C5	
PT	component - to inhibit complement induced cell lysis	
PS	Claim 24; Page 107-110; 10pp. English.	
CC	DNA (1084479) coding for murine scFv 5G1.1M1 (R77606) was obt'd. by	
CC	PCR cloning of DNA from hybridoma ATCC HB 11625, the producer of	
CC	anti-C5 monoclonal antibody (MAB) 5G1.1. The DNA was subcloned into	
CC	pET rec S05/MI for expression in Escherichia coli. The light and/or	
CC	heavy chain CDRs of scFv 5G1.1M1 can be combined with CDRs from other	
CC	5G1.1-derived antibodies, Fds and light chains (R77607-16) in the	
CC	prodn. of recombinant, including humanised, antibodies that retain	
CC	the ability of MAb 5G1.1 to block human complement C5a generation	
CC	and thus to reduce glomerular inflammation and kidney dysfunction	
CC	associated with glomerulonephritis.	
SO	Sequence 747 BP; 183 A; 174 C; 211 G; 179 T;	

Query Match	53.18;	Score 396.6;	DB 1;	Length 747;
Best Local Similarity	70.78;	Pred. No. 2e-101;		
Matches 528;	Conservative 0;	Mismatches 219;	Indels 0;	Gaps 0;

OY	1	ATGGCGGATATTCAGAGTAGACCACTCCCGGCTCCCTGGTCCGGCTGTGGGGGAGTAGG	60
Db	1	ATGGCCGACATCCAGATGATGACTGCTTCACGCTTCACTGTGTGCATGTGGGGGAAACT	60
OY	61	GTCACCATCACCTCGGGCGCCAGCGAAACATCTATGGCGCGCGGAAGCTGGTATCAAGT	120
Db	61	GTCACCATCACATGATGGAGGACAGTAGAATATTAGGTGGTTTAAATGGTATCACGGG	120
OY	121	AAACCTGGGAAAAGCTCCGAGACTTCTGATTTACGCTGCGAAGAACTGGCAGATGAGTC	180
Db	121	AAACAGGGAAATATCTCCACACTCTCTGATCTATGTGTCAACCAACTGGCAGATGGCATG	180
OY	181	CCTTTCGCTCTCTCGATCCGGCTCGGCGGAAACGGAATTCACTGACATCAGACAGCTG	240
Db	181	TCATCGAGGTTCACTGGCAGTGGATCTGCTGTAAGACATATTATCCAAAGATCAGTAGCTG	240
OY	241	CAGCGTGAAGACTTCGCTACGATATTACTGTGCAGACGTTTTAAATACCTCGGTGACTTC	300
Db	241	CATCGCTGACGATGTGTGACAGCTATTACTGTCAAAATGTGTTAAATACTCCTCAGCTTC	300
OY	301	GGACAGGATACCAAGGTGGAATAAAACGTACTGCGGTGGTGTCTGCTGGCGGTGA	360
Db	301	GGTGTGGGACCAAGTTGAGACTGAAACGACCGAGATGGCGGGTCTGGGTGGCGGGGA	360
OY	361	TCTGTGGTGGCGGTTCCAAAGTCCAACTGGTGCATCCGCGCCGCGAGGCTCAAGAACCA	420
Db	361	TGGGTGGCGGAGGATCGCAAGTTCACTGTGACGACAGTCTGGAGCCGAGCTGAATAACTT	420
OY	421	GGGGCTCATGTCAAAGTGTCCCTGTAAAGCTAAGCGCTATATTTTCTTAATTAATGGATT	480
Db	421	GGGGCTCATGTAAGATGTCTGCAAGGCTACTGCTACATATTCAGTAACACTACTGATA	480
OY	481	CAATGGGTGCTCAGGCCCCCGGGCAGGGCTGGATATGATGGGTGAGATCTTACCGGGC	540
Db	481	CAGTGGATPAAAGCAGAGGCGCTGGACATAGCCCTTGAAGTGATGGTGAGATTTAACCGGA	540
OY	541	TCTGTGACACCGAATATACGAAATTTTAAAGACCGGTGTACTATAGACCGGTGACACT	600
Db	541	AGTGGTCTACTGTAGTACACTGAAACCTTCAAGGACAGGCGCGGATTCAGTGCAGATACA	600

[illegible]

RESULT

ID	T08484	standard; DNA; 750 BP.
AC	T08484;	
DT	02-APR-1996	(first entry)
DE	Humanised 5G1.1 VH + IGHRC DNA.	
KW	Complement C5; haemolysis; kidney; glomerulonephritis;	
KW	monoclonal antibody; antiinflammatory; antibody engineering;	
KW	humanised antibody; complementarity determining region; CDR;	
KW	ds.	
OS	Synthetic.	
PH	Key	
FT	cds	Location/Qualifiers
FT		1..750
FT	/*tag-	a
FT	signal_peptide	1..57
FT	/*tag-	b
FT	mat_peptide	58..747
FT	/*tag-	c
PN	W09529697-A1.	

	Query Match	Best Local Similarity	Matches 377: Conservative	49.7%: Score 371; DB 1; Length 750; 97.4%: Pred. No. 2.7e-94;	0: Mismatches 10; Indels 0; Gaps 0;
PF	01-MAY-1995; U05688.				
PR	02-MAY-1994; U5-236208.				
PA	(ALEX-) ALEXION PHARM INC.				
PI	Evans MJ, Mattis L, Mueller EE, Nye SH, Rollins S;				
PI	Rother RP, Springhorn J P, Squinto SP, Thomas TC;				
PI	Mang Y, Wilkins JA;				
DR	WPI: 95-392923/50.				
DR	P-PSDB: R77611.				
PT	Treating glomerulonephritis with antibody against complement C5				
PT	component - to inhibit complement induced cell lysis				
PS	Claim 38: Page 123-125; 181pp: English.				
CC	A DNA construct (T08483) codes for a humanised CDR-grafted and				
CC	framework sequence-altered Fd 5G1.1 VH + IgRL (R77610), which				
CC	includes CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1.				
CC	The DNA can be subcloned together with DNA (T08484) coding for a				
CC	humanised light chain (R77612) into vector APEX-3P (T08476) for				
CC	expression of humanised antibody in human 293 EBNA cells. Such				
CC	recombinant antibodies retain the ability of Mab 5G1.1 to block				
CC	human complement C5a generation and thus to reduce glomerular				
CC	inflammation and kidney dysfunction associated with				
CC	glomerulonephritis.				
SS	Sequence 750 BP; 163 A; 220 C; 197 G; 170 T;				
QY	358 GGAATGTGGTGGGGGGGGTCTCAAGTCACACAGTGGTCATCCGGGCGGACGAAGAAG	417			
DB	37 GTAATCGCCGGGGTCCACTCTCCAAGTCCACACTGGTGCATTCGGGCGCCAGGTCAAGAAG	96			
QY	418 CCAGGGGCGCTCAGTCAAAAGTGTCTGTAAAGCTAGCGGCTATATTTTCTAATTAATGG	477			
DB	97 CCAGGGGCGCTCAGTCAAAAGTGTCTGTAAAGCTAGCGGCTATATTTTCTAATTAATGG	156			
QY	478 ATTCAATGGGTGCTGCACAGGCCCCCGGGGACGGGCTGTGAATGCATGGGTGAGATCTTACCG	537			
DB	157 ATTCAATGGGTGCTGCACAGGCCCCCGGGGACGGGCTGTGAATGCATGGGTGAGATCTTACCG	216			


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QY 418 CAGAGGCGCTGATCAAAAGTCTCTGTAAGCTAGCGCTATATTTTCTAATTATGG 477
      |||
      97 CAGAGGCGCTGATCAAAAGTCTCTGTAAGCTAGCGCTATATTTTCTAATTATGG 156
QY 478 ATTCAAAGGCGCTGACGAGGCGCGGAGAGGCGCTGGAATGGATGGAGATCTTACG 537
      |||
      157 ATTCAAAGGCGCTGACGAGGCGCGGAGAGGCGCTGGAATGGATGGAGATCTTACG 216
QY 538 GCGCTGTGTAGACACGGAATATACGAAATTTTAAGACCGGTACTATGACGCGTGAC 597
      |||
      217 GCGCTGTGTAGACACGGAATATACGAAATTTTAAGACCGGTACTATGACGCGTGAC 276
QY 598 ACTTCGACTAGTACAGTATATGAGAGTCTTCAGACCTGCGATCGAGACAGCGCGTC 657
      |||
      277 ACTTCGACTAGTACAGTATATGAGAGTCTTCAGACCTGCGATCGAGACAGCGCGTC 336
QY 658 TATTATGCGCGCGCTATATTTTGGTCTAGCCCGAATGGTATTTGATGTTGGGGT 717
      |||
      337 TATTATGCGCGCGCTATATTTTGGTCTAGCCCGAATGGTATTTGATGTTGGGGT 396
QY 718 CAAGAACCTGTGCTACTGTCTGAGC 744
      |||
      397 CAAGAACCTGTGCTACTGTCTGAGC 423
      |||

RESULT 7
T10706
ID T10706 standard; DNA: 726 BP.
AC T10706;
DE 02-APR-1996 (first entry)
DE Humanised 5G1.1 VL + KLV56B DNA.
KM Complement C5; haemolysis; kidney; glomerulonephritis;
KM monoclonal antibody; antiinflammatory; antibody engineering;
KM humanised antibody; complementarity determining region; CDR;
KM ds.
OS Synthetic.
FH Key Location/Qualifiers
FT cds 1..726
FT signal_peptide 1..75
FT mat_peptide 76..723
FT mat_peptide /*tag= b
FT mat_peptide /*tag= c
PN WO9529697-A1.
PD 09-NOV-1995.
PF 01-MAY-1995; U05688.
PR 02-MAY-1994; US-236208.
PA (ALEX-) ALEXION PHARM INC.
PI Evans MJ, Matlis L, Mueller EE, Nye SH, Rollins S;
PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;
PI Wang Y, Wilkins JA;
PI WPI: 95-392923/50.
DR P-PSDB: R77613.
PT Treating glomerulonephritis with antibody against complement C5
PT component - to inhibit complement induced cell lysis
PS Claim 42; Page 129-131; 181pp; English.
CC A DNA construct (T10706) codes for a humanised CDR-grafted and
CC framework sequence-altered light chain, 5G1.1 VL + KLV56B (R77613),
CC which includes CDRs derived from mouse anti-C5 monoclonal antibody
CC 5G1.1. The DNA can be subcloned together with DNA (T08483) coding
CC for a humanised Fd (R77610) into vector APEX-3P (T08476) for
CC expression of humanised antibody in human 293 EBNA cells. Such
CC recombinant antibodies retain the ability of MAb 5G1.1 to block
CC human complement C5a generation and thus to reduce glomerular
CC inflammation and kidney dysfunction associated with
CC glomerulonephritis.
SQ Sequence 726 BP; 175 A; 206 C; 187 G; 158 T;
```

```
QY 2 TGGCCGATATCAGATGACCCAGTCCCTCTCCCTGTCGGCTGTGGCGATAGGG 61
      |||
      77 TCAGAGATATCAGATGACCCAGTCCCTCTCCCTGTCGGCTGTGGCGATAGGG 136
QY 62 TCACATACCTCGGCGCCGACGAGAAATCATATGCGCGCTGAGACTGATCAACGTA 121
      |||
      137 TCACATACCTCGGCGCCGACGAGAAATCATATGCGCGCTGAGACTGATCAACGTA 196
QY 122 AACCTGGGAAGCTCCGAGCTTCTGATTACGCTCGACGAAACCTGGCAGATGAGTCC 181
      |||
      197 AACCTGGGAAGCTCCGAGCTTCTGATTACGCTCGACGAAACCTGGCAGATGAGTCC 256
QY 182 CTTCCTGCTTCTCTGATCCGCTCCGAAACGATTTCACTGACCATCAGCAGTTCG 241
      |||
      257 CTTCCTGCTTCTCTGATCCGCTCCGAAACGATTTCACTGACCATCAGCAGTTCG 316
QY 242 AGCTGAAACCTTCGCTACGATTTACTGTCAGAACCTTTAAATACTCCGTTGACTTG 301
      |||
      317 AGCTGAAACCTTCGCTACGATTTACTGTCAGAACCTTTAAATACTCCGTTGACTTG 376
QY 302 GACAGGCTACCAAGTGGAATAAACGTAAGTGGCGGTGGTGTCTG 349
      |||
      377 GACAGGCTACCAAGTGGAATAAACGTAAGTGGCGGTGGTGTCTG 424
      |||

RESULT 8
T08486
ID T08486 standard; DNA: 711 BP.
AC T08486;
DE 15-MAR-1996 (first entry)
DE Humanised 5G1.1 VL + 012 DNA.
KM Complement C5; haemolysis; kidney; glomerulonephritis;
KM monoclonal antibody; antiinflammatory; antibody engineering;
KM humanised antibody; complementarity determining region; CDR;
KM ds.
OS Synthetic.
FH Key Location/Qualifiers
FT cds 1..711
FT signal_peptide 1..66
FT mat_peptide 67..708
FT mat_peptide /*tag= a
FT mat_peptide /*tag= b
FT mat_peptide /*tag= c
PN WO9529697-A1.
PD 09-NOV-1995.
PF 01-MAY-1995; U05688.
PR 02-MAY-1994; US-236208.
PA (ALEX-) ALEXION PHARM INC.
PI Evans MJ, Matlis L, Mueller EE, Nye SH, Rollins S;
PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;
PI Wang Y, Wilkins JA;
PI WPI: 95-392923/50.
DR P-PSDB: R77614.
PT Treating glomerulonephritis with antibody against complement C5
PT component - to inhibit complement induced cell lysis
PS Claim 35; Page 132-34; 181pp; English.
CC A DNA construct (T08486) codes for a humanised CDR-grafted
CC light chain, designated 5G1.1 VL + 012 (R77614), which includes
CC CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1. The
CC DNA can be subcloned together with DNA (T08484) coding
CC for a humanised Fd (R77611) into vector APEX-3P (T08476) for
CC expression of humanised antibody in human 293 EBNA cells. Such
CC recombinant antibodies retain the ability of MAb 5G1.1 to block
CC human complement C5a generation and thus to reduce glomerular
CC inflammation and kidney dysfunction associated with
CC glomerulonephritis.
SQ Sequence 711 BP; 174 A; 206 C; 183 G; 148 T;
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Query Match 44.0%; Score 328.8; DB 1; Length 726;
Best Local Similarity 96.6%; Pred. No. 1.5e-82;
Matches 336; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Query Match 43.3%; Score 323.8; DB 1; Length 711;
Best Local Similarity 96.5%; Pred. No. 3.6e-81;
Matches 331; Conservative 0; Mismatches 12; Indels 0; Gaps 0;


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QY 7 GATATCCAGATGACCCAGTCCCGTCCCTGTCCTGTCGGCGATAGGTCACC 66
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Db 67 GATATCCAGATGACCCAGTCCCGTCCCTGTCCTGTCGGCGATAGGTCACC 126
  |||
QY 67 ATCACTGCGCGCCAGCAAGAACATCTATGCGCGCTGAACCTGTATCAACGTAACCT 126
  |||
Db 127 ATCACTGCGCGCCAGCAAGAACATCTATGCGCGCTGAACCTGTATCAACGTAACCT 186
  |||
QY 127 GGAAGAGCTCCGAGCTCTGATTTACGTCGGTGGAGAACCTGGCAGATGGAGTCTTCT 186
  |||
Db 187 GGAAGAGCTCCGAGCTCTGATTTACGTCGGTGGAGAACCTGGCAGATGGAGTCTTCT 246
  |||
QY 187 CGCTTCTCTGATCCGCGTCCGGAACGATTTCACTCTGACCATCAGCAGCTTCGAGCT 246
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Db 247 CGCTTCTCTGATCCGCGTCCGGAACGATTTCACTCTGACCATCAGCAGCTTCGAGCT 306
  |||
QY 247 GAAGACTTCGCTAGCTATTTACTGTCAGAACGCTTTTAAATACCTCCGTTTCGAGAC 306
  |||
Db 307 GAAGACTTCGCTAGCTATTTACTGTCAGAACGCTTTTAAATACCTCCGTTTCGAGAC 366
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QY 307 GGTACCAAGGTGGAAATAAAGCTACTGCGGTGGTGGTCTTG 349
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Db 367 GGTACCAAGGTGGAAATAAAGCTACTGCGGTGGTGGTCTTG 409
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RESULT 9

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Q20485
ID T08485 standard; DNA; 726 BP.
AC T08485;
DT 15-MAR-1996 (first entry)
DE Humanised 5G1.1 VL + KLV56 DNA.
KW Complement C5; haemolysis; kidney; glomerulonephritis;
KW monoclonal antibody; antiinflammatory; antibody engineering;
KW humanised antibody; complementarity determining region; CDR;
KW ds.
OS Synthetic.
FH Key Location/Qualifiers
FT cds 1..726
FT signal_peptide 1..75 /*tag= a
FT mat_peptide 76..723 /*tag= b
FT mat_peptide 76..723 /*tag= c
PN WO9529697-A1.
PD 09-NOV-1995.
PF 01-MAY-1995; U05688.
PR 02-MAY-1994; US-236208.
PA (ALEX-) ALEXION PHARM INC.
PI Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S;
PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;
PI Wang Y, Wilkins JA;
PI WPI; 95-392923/50.
DR P-PSDB; T08485.
DR Treating glomerulonephritis with antibody against complement C5
PT component - to inhibit complement induced cell lysis
PS Example 11; Page 126-128; 181pp; English.
CC A DNA construct (T08485) codes for a humanised CDR-grafted and
CC framework sequence-altered light chain, 5G1.1 VL + KLV56 (R77612),
CC which includes CDRs derived from mouse anti-C5 monoclonal antibody
CC 5G1.1. The DNA can be subcloned together with DNA (T08483) coding
CC for a humanised Fd (R77610) into vector APEX-3P (T08476) for
CC expression of humanised antibody in human 293 EBNA cells. Such
CC recombinant antibodies retain the ability of MAb 5G1.1 to block
CC human complement C5a generation and thus to reduce glomerular
CC inflammation and kidney dysfunction associated with
CC glomerulonephritis.
SQ Sequence 726 BP; 176 A; 207 C; 186 G; 157 T;

Query Match 43.2%; Score 322.4; DB 1; Length 726;
Best Local Similarity 95.4%; Pred. No. 8.9e-81;
Matches 332; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
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Db 77 TGCAGGATATCCAGATGACCCAGTCCCGTCCCTGTCCTGTCGGCGATAGGG 136
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QY 62 TCACCATCACTTCGCGCGCCAGCAAGAACATCTATGCGCGCTGAACCTGTATCAACGTA 121
  |||
Db 137 TCACCATCACTTCGCGCGCCAGCAAGAACATCTATGCGCGCTGAACCTGTATCAACGTA 196
  |||
QY 122 AACCTGGGAAGCTCCGAAGCTTCGATTTACGTCGGTGGAGAACCTGGCAGATGGAGTCC 181
  |||
Db 197 AACCTGGGAAGCTCCGAAGCTTCGATTTACGTCGGTGGAGAACCTGGCAGATGGAGTCC 256
  |||
QY 182 CTTCTCTCTCTGATCCGCGTCCGGAACGATTTCACTCTGACCATCAGCAGTCTGC 241
  |||
Db 257 CTTCTCTCTCTGATCCGCGTCCGGAACGATTTCACTCTGACCATCAGCAGTCTGC 316
  |||
QY 242 AGCCTGAAGACTTCGCTAGCTATTTACTGTCAGAACGCTTTTAAATACCTCCGTTGACTTTCG 301
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Db 317 AACCTGAGGACTTCGCTAGCTATTTACTGTCAGAACGCTTTTAAATACCTCCGTTGACTTTCG 376
  |||
QY 302 GACAGGTACCAAGGTGGAAATAAAGCTACTGCGGTGGTGGTCTTG 349
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Db 377 GACAGGTACCAAGGTGGAAATAAAGCTACTGCGGTGGTGGTCTTG 424
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RESULT 10

```
Q20381
ID Q20381 standard; DNA; 819 BP.
AC Q20381;
DT 15-APR-1992 (first entry)
DE Sequence encoding the shortened hinge version of the B72.3 single
DE chain Fv hinge.
KW Fv fragment; in vivo diagnosis; therapy; antibody; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 1..816 /*tag= a
FT WO9119739-A.
PN 26-DEC-1991.
PD 11-JUN-1991; G00935.
PR 11-JUN-1990; GB-012995.
PA (CELL-) CELLSOURCE LTD.
PI King DJ, Mountain A, Owens RJ, Yarranton GT;
PI WPI; 92-024365/03.
DR P-PSDB; R20185.
DR New multivalent antigen-binding proteins - comprise Fv fragment
PT linked to at least 1 other Fv fragment spacer and useful for
PT in-vivo diagnosis or therapy
PS Example; Fig 5 54pp; English.
CC The bivalent antigen-binding protein B72.3 Fv (R20184) is an example
CC of the antigen-binding proteins of the invention. They comprise a
CC first Fv fragment bound to at least one other Fv fragment by a
CC linker which keeps the Fv fragment apart. The connecting structure
CC of R20184 comprises a joining sequence derived from a human IgG1
CC domain linked to a complete human IgG4 hinge region. R20185 is the
CC sequence of the shortened hinge version of the B72.3 single chain Fv
CC hinge.
SQ Sequence 819 BP; 218 A; 198 C; 214 G; 189 T;

Query Match 39.4%; Score 294; DB 1; Length 819;
Best Local Similarity 66.3%; Pred. No. 7.5e-73;
Matches 439; Conservative 0; Mismatches 220; Indels 3; Gaps 1;
```

```
QY 4 GCGGATATCCAGATGACCCAGTCCCGTCCCTGTCCTGTCGGCGATAGGGTC 63
  |||
Db 64 GCGGATATCCAGATGACCCAGTCCCGTCCCTGTCCTGTCGGCGATAGGGTC 123
  |||
QY 64 ACCATCACTTCGCGCGCCAGCAAGAACATCTATGCGCGCTGAACCTGGTATCAACGTA 123
  |||
Db 124 ACCATCACTTCGCGCGCCAGCAAGTATGAGATATTTACAGTAATTTACCATGGTATCAACAGAA 183
  |||
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OY	124	CTGGGAAGCTCCGAACTCTCTATTTACGTGCGAGCAACCTGGCGAGATGGAGTCCCT	183
Db	184	CAGGAAAATCTCCTCAGACTCTCTGTCTATCTCTCAACAACTTAGAGATGGTGGCCA	243
OY	184	TCTGCTTCTCTGGATCCGGCTCCGAAACGGATTCTCACTGTACCATCAGCAGTGTCCAG	243
Db	244	TCAAGTTCAGTGGGAGTGGATCGGGGACACAGTATTCCTCAAGATTCACACGCTGACG	303
OY	244	CCTGAAGCTTCGCTACGTATTACTGTGCAGACCTTTTAAATACTCCGTTGACTTGGGA	303
Db	304	TCTGAAGATTTTGGAGATTATTACTGTCAACATTTTGGGGTACTCCGTACACGTTGGGA	363
OY	304	CAGGTACCAAGGTGGAAATTAACGATACCTGCGGTGTGGTCTGGTGGCGGTGATCT	363
Db	364	GGGGGACCAAGCTTTGAATATTAACG---TGTGTGGCGGGGATCTCCGGCGGGGAGGTTCA	420
OY	364	GGTGTGGCGGTCTTCAAGTCCAACTGGTGCATCTCCGGCCGAGGTCAAGAACCCAGGG	423
Db	421	GGGGGTGGCGGATCCAGAGTTCACTCGACGACGATCTACCTAGTGGTGGAAACCTGGG	480
OY	424	GCCTCAGTCAAAAGTGTCTCTGTAAAGCTAGCGGGCTAATTTTCTAATTAATTGGATTCAA	483
Db	481	GCTTCAGTGAAGATATCTCTCGAAGGCTTCTGGCTACACTTCACTGACCACTGATTTAC	540
OY	484	TGGGTGCTCAAGGCCCCCGGCGAGGGCTGTGAATGATGGGTAGATCTTACCGGGCTCT	543
Db	541	TGGGGGAAGCAAGACCTCGAACAAGGGCTGTGAATGATGGATATATTCTCCCGGAAT	600
OY	544	GGTAGCACCGAATATACGAAATTTTAAAGACCGGTGTACTATAGACGCTGACACTTCG	603
Db	601	GATGATATTAGTTCOAATGAAATTTCAAGGGCAAGCCACACTGACTGAGACCAATTC	660
OY	604	ACTAGTACGTAATACATGAGACTTCCAGCCTGCGATCGAGACGACGCGGCTCTAATTAT	663
Db	661	TCCAGCACTGCTACATGACACTCAACAGCCTGCATCTGAGGATTTGCGAGTGTATTTC	720
OY	664	TG 665	
Db	721	TG 722	

RESULT 11

042284

ID Q42284 standard; cDNA; 723 BP.

AC Q42284;

DT 13-SEP-1993 (first entry)

DE V-((kappa)/[(Gly)4Ser]3/V-(gamma)) single chain antibody.

RV Type I ribosome-inactivating protein; ricin; gelonin;

KW immunoenzyme; autolysosomal disease; cell killing; toxin;

KW overlap extension polymerase chain reaction; H65 variable region;

KW RMA; rabbit muscle aldolase; cathepsin cleavage;

SL: E.coli Shiga-like toxin; human engineered antibody; ss.

OS Synthetic.

PN MO309130-A.

PD 13-MAY-1993.

PF 04-NOV-1992; 009487.

PR 04-NOV-1991; US-787567.

PR 19-JUN-1992; US-901707.

PA (XOMA) XOMA CORP.

PI Behard SL, Better MD, Carroll SF, Lane JA, Let SP;

DR WP; 93-167617/20.

PT Analogs of type I ribosome inactivating protein - useful as

PT cytotoxic agents, immuno toxins for treating auto immune diseases,

PT Example 12; Page 123-124; 163pp; English.

CC A single chain antibody form of the he3 H65 variable domain was

CC assembled from previously constructed genes. This scab segment

CC consisted of the entire V and J region of one chain (heavy or

CC light) linked to the entire V and J segment of the other (light or

CC heavy) via a 15 amino acid flexible peptide. The scab was assembled

CC in two orientations (see Q42284 and Q42285). A fusion construct was

CC prepared in which the natural sequence gelonin gene was positioned

CC at the N-terminus and the SLT or RMA linker peptide was positioned

CC between the gelonin and scAb domains.	
Sequence	723 BP; 178 A; 162 C; 207 G; 176 T;
5'	
3'	

Query Match	37.9%	Score 283.4	DB 1	Length 723
Best Local Similarity	63.7%	Pred. NO. 6.4e-70		
Matches 472; Conservative	0	Mismatches 251	Indels 18	Gaps 2

Oy	7	GATATCCAGATGACCACTCCCCTCCCTCCTGTGCCGTGTGGCGAATAGGGTCACC	66
Dd	1	GACATCCAGATGACTCACTCTCCATCTTCCCTGTCTGCATCTGTAGAGACAGATCACT	60
Oy	67	ATCACCTCGGGCGCCAGCGAAACAATCTATGCGCGCTGAACCTGGATCAACGTAAACT	126
Dd	61	ATCACTTCCCGGGGAGATCAGSACATTAAATGATTAATTAACTGGTTCCACAGAACCA	120
Oy	127	GGGAAAGCTCCGAAAGCTTCTATTTACGGGTGCGACGAACCTGGCAGATGAGTGCCCTCT	186
Dd	121	GGGAAAGCTCCTTAGAGACCTCATCTATCTGTCACAAACAGATTGGATCTGGGGTCCCATCA	180
Oy	187	CGCTTCTGTGATCGGCTCCGGAAACGGAATTTCACTGACATCAGACAGTCTCACACT	246
Dd	181	AGGTTCACTGGCAGTGGATCTGGGACAGATTAATCTCTACACATCAGACGCTTCAAAT	240
Oy	247	GAAAGCTTCGCTAGATTAATTACTGTGCAGAAGCTTTAAATACTCCGTTGACTTTGGACAG	306
Dd	241	GAAAGTTTTGGAAATTTATTAATTATGTCCACAGATATGATGATGCTCCGTGGAGCTGGTGA	300
Oy	307	GGTACCAAGGTGGAAATTAACACACTACTGCGCGTGTGTTTGTGTGGCGGTGATCTGCT	366
Dd	301	GGCACCAAGCTTGAGATMAA-----GGTGGCGGTGATCTGGTGGAGGTGGGTCCGGA	354
Oy	367	GGTGGCGGTTCCTCAAGTCCCACTGGTGCATCCGGCGCGAGGTCAAGAACCCAGGGGCC	426
Dd	355	GGTGGAGGATCTGAGATCCAATGCTGGTGCATCTGGAGAGCGCTGGTGAACCTGGAGGG	414
Oy	427	TCAGTCAAAAGTGTCTCTGTAAGACTAGCGGCTAATATTTTCTTAATTATGGATTCAAATG	486
Dd	415	TCCGTCAAAATCTCCTCGGACGCTTCTGGTATACCTTCACAAACATAATGAAATGAATGG	474
Oy	487	GTGCGTCAGGCCCGCGGACAGGGCCTGSAATGATGGTGAATCTTAACCGGGCTCTGCT	546
Dd	475	GTGCCCCAGGCTCCAGAGAAAGGGTTAGAGTGATGGGCTGGGAATAAACACCCACACTGGA	534
Oy	547	AGCACGGAATPACGAAAATTTTAAAGACCGGTGTATATGACGCGGTGACACTTGACT	606
Dd	535	GAGCCAAATATGCTGATCTTTCAAGGAGAGGTTTACCTTCTCTTTGGACGATTTCAAG	594
Oy	607	AGTACAGTATACATGAGACCTCTCAGCCTGCGATCGAGAGACAGCGCGCTATATTATTC	666
Dd	595	AACACTGCTTATTAACAGATCAACAGCCTCAGAGCGGAGACAGGGCTGTATTTCTGT	654
Oy	667	GCGCGTATTTTGTGGTTCAGCCCGAATTGGTATTTGATGTTTGGGGTCAAGGAAC	726
Dd	655	ACAAACAGGGGTATAG-----ACTGTACTTCGATGTCTGGGCGCAAGGAGCC	702
Oy	727	CTGTCACACTGTGAGCTGA 747	
Dd	703	ACGGTCACCGTCTCTCATGA 723	
RESULT	12		
ID	T94963		
AC	T94963 standard; DNA; 1065 BP.		
DT	20-APR-1998 (first entry)		
DE	R. pipiens recombinant Rñse rOnc fusion protein 1 DNA.		
KW	Rñse A: ribonuclease; cytotolic; onconase; nOnc; immunofusion;		
OS	tumour cell growth; frog; ss.		
OS	Rana pipiens.		
OS	Synthetic.		
PN	WO9731116-A2.		
PD	28-AUG-1997.		

PF 19-FEB-1997; U02588.
PR 21-FEB-1996; US-011800.
PI (USSH) US DEPT HEALTH & HUMAN SERVICES.
DR Boque L, Newton DL, Rybak SM, Wlodawer A;
WPI: 97-435168/40.
DR P-PSDB; W35125.
PT Ribonuclease molecules based on native Onconase - used for killing
PT cells, particularly tumour cells
PS Disclosure; Page 67; 90pp; English.
CC Sequences T94963 to T94973 encode recombinant fusion proteins (rOnc)
CC which are modifications of the RNase Onconase (RTM) (nOnc). Such novel
CC ribonuclease molecules are highly cytotoxic and can be used alone or
CC to form chemical conjugates or to target recombinant immunofusions. They
CC are used particularly for decreasing tumour cell growth. They can also be
CC used for cell separation in vitro by selectively killing unwanted types
CC of cells, e.g. in bone marrow prior to transplantation into a patient
CC undergoing marrow ablation by radiation, or for killing leukaemia cells
CC or T-cells that would cause graft versus host disease. The toxins can
CC also be used to selectively kill unwanted cells in culture. The new
CC ribonucleases have increased cytotoxic activity compared to nOnc and also
CC lower immunogenicity in humans. 240 C; 252 G; 272 T;
SQ Sequence 1065 BP; 301 A; 240 C; 252 G; 272 T;

Query Match 35.7%; Score 267; DB 1; Length 1065;
Best Local Similarity 63.4%; Pred. No. 2.7e-65;
Matches 427; Conservative 0; Mismatches 240; Indels 6; Gaps 1;

QY 7 GATATCCAGATGACCCAGTCCCGTCCCTGCTGCGGCTCTGTGGGCGATAGGTCACC 66
DB 1 GACATCAAGATGACCCAGTCCCTGCTGCGGCTCTGTGGGCGATAGGTCACC 60
QY 67 ATCACTCGCGGCGCCAGGAAACATCTATGCGCGCTGAACGTGTATCAACGTTAAACCT 126
DB 61 TTCATTGCAAGCGAGTCAGGACATTAATACTATTATGTCGCTCCAGCAAGAACCA 120
QY 127 GGAAGAGCTCCGAAGCTTCTGATTTACGGTGGGACGAACCTGGCAGATGGAGTCCCTTCT 186
DB 121 GGAAGATCTCCGAAGCTTCTGATTTACGGTGGGACGAACCTGGCAGATGGAGTCCCTTCT 180
QY 187 GGTGGCGGTCTCAAGTCCAACTGGTGCAATCCGGCGCGGAGTCAAGAGCCAGGGGCC 426
DB 355 GCGGCGGCTCTGAGTTTCAGCTCCAGCAGTCTGAGCAGTCTACTTGGCAAGGCCCTGGGGCT 414
QY 427 TCAGTCAAAGTGTCTCTGTAAGCTACCGGCTATATTTTCTTAATTATTGGATTCAATGG 486
QY 667 GCGGGTATTATTTT 679

DB 655 ACCCTCTTTATT 667
RESULT 13
T94967
ID T94967 standard; DNA; 1065 BP.
AC T94967;
DT 20-APR-1998 (first entry)
DE R. pipiens recombinant RNase rOnc fusion protein 5 DNA.
KW RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion;
KW tumour cell growth; frog; ss.
OS Rana pipiens.
OS Synthetic.
PN W09731116-A2.
PD 28-AUG-1997; U02588.
PF 19-FEB-1997; U02588.
PR 21-FEB-1996; US-011800.
PI (USSH) US DEPT HEALTH & HUMAN SERVICES.
PI Boque L, Newton DL, Rybak SM, Wlodawer A;
DR WPI: 97-435168/40.
DR P-PSDB; W35129.
PT Ribonuclease molecules based on native Onconase - used for killing
PT cells, particularly tumour cells
PS Disclosure; Page 71; 90pp; English.
CC Sequences T94963 to T94973 encode recombinant fusion proteins (rOnc)
CC which are modifications of the RNase Onconase (RTM) (nOnc). Such novel
CC ribonuclease molecules are highly cytotoxic and can be used alone or
CC to form chemical conjugates or to target recombinant immunofusions. They
CC are used particularly for decreasing tumour cell growth. They can also be
CC used for cell separation in vitro by selectively killing unwanted types
CC of cells, e.g. in bone marrow prior to transplantation into a patient
CC undergoing marrow ablation by radiation, or for killing leukaemia cells
CC or T-cells that would cause graft versus host disease. The toxins can
CC also be used to selectively kill unwanted cells in culture. The new
CC ribonucleases have increased cytotoxic activity compared to nOnc and also
CC lower immunogenicity in humans. 241 C; 250 G; 273 T;
SQ Sequence 1065 BP; 301 A; 241 C; 250 G; 273 T;

Query Match 35.7%; Score 267; DB 1; Length 1065;
Best Local Similarity 63.4%; Pred. No. 2.7e-65;
Matches 427; Conservative 0; Mismatches 240; Indels 6; Gaps 1;

QY 7 GATATCCAGATGACCCAGTCCCGTCCCTGCTGCGGCTCTGTGGGCGATAGGTCACC 66
DB 1 GACATCAAGATGACCCAGTCCCTGCTGCGGCTCTGTGGGCGATAGGTCACC 60
QY 67 ATCACTCGCGGCGCCAGGAAACATCTATGCGCGCTGAACGTGTATCAACGTTAAACCT 126
DB 61 TTCATTGCAAGCGAGTCAGGACATTAATACTATTATGTCGCTCCAGCAAGAACCA 120
QY 127 GGAAGAGCTCCGAAGCTTCTGATTTACGGTGGGACGAACCTGGCAGATGGAGTCCCTTCT 186
DB 121 GGAAGATCTCCGAAGCTTCTGATTTACGGTGGGACGAACCTGGCAGATGGAGTCCCTTCT 180
QY 187 GGTGGCGGTCTCAAGTCCAACTGGTGCAATCCGGCGCGGAGTCAAGAGCCAGGGGCC 426
DB 355 GCGGCGGCTCTGAGTTTCAGCTCCAGCAGTCTGAGCAGTCTACTTGGCAAGGCCCTGGGGCT 414
QY 427 TCAGTCAAAGTGTCTCTGTAAGCTACCGGCTATATTTTCTTAATTATTGGATTCAATGG 486

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Db 415 TCAGTGAAGATGCTCGAAGGCTTCTGGCTACACCTTTCCAGCTACGATGACCTGG 474
QY 487 GTGGCTAGGCCCGGCGGCGCTGGAATGATGAGATCTTACCGGCTCTGGT 546
Db 475 ATAAACAGAGGCGCTGACAGGCTGTGACGTGATGCTGATGATCTTGAATTAAT 534
QY 547 AGCACCAGATATACGAAATTTTAAAGACCGTGTACTATGACCGGTGACACTTGACT 606
Db 535 GATACATATTATCAACCCCAATTCACCAAGGCCAAACCTAGCTGACACTCCACCC 594
QY 607 AGTACAGATATACATGAGACTCTCCAGCTGCGATGCGAGAGAACGGCCCTATTATTCC 666
Db 595 AGCACTGCTACATGGAAGCTCAACAGCCTGACCAATGAGGACTCTGCGGTCTATTACTGT 654
QY 667 GCGGCTATTATTT 679
Db 655 ACCCCTTTATT 667

RESULT 14
T94965
ID T94965 standard; DNA; 1074 BP.
AC T94965; 1998 (first entry)
DE R. pipiens recombinant RNase ronc fusion protein 3 DNA.
KW RNase A; ribonuclease; cytotoxic; onconase; nonc; immunofusion;
KM tumour cell growth; frog; ss.
OS Rana pipiens.
OS Synthetic.
PN WO9731116-A2.
PD 28-AUG-1997.
PF 19-FEB-1997; U02588.
PR 21-FEB-1996; US-011800.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PI Bogue L, Newton DL, Rybak SM, Wlodawer A;
DR WPI; 97-435168/40.
DR P-PSDB; W35127.
PT Ribonuclease molecules based on native Onconase - used for killing
PT cells, particularly tumour cells.
PS Disclosure; Page 69; 90pp; English.
CC Sequences T94963 to T94973 encode recombinant fusion proteins (rOnc)
CC which are modifications of the RNase Onconase (RNM) (nonc). Such novel
CC ribonuclease molecules are highly cytotoxic and can be used alone or
CC to form chemical conjugates or to target recombinant immunofusions. They
CC are used particularly for decreasing tumour cell growth. They can also be
CC used for cell separation in vitro by selectively killing unwanted types
CC of cells, e.g. in bone marrow prior to transplantation into a patient
CC undergoing marrow ablation by radiation, or for killing leukaemia cells
CC or T-cells that would cause graft versus host disease. The toxins can
CC also be used to selectively kill unwanted cells in culture. The new
CC ribonucleases have increased cytotoxic activity compared to nonc and also
CC lower immunogenicity in humans.
SQ Sequence 1074 BP; 304 A; 246 C; 250 G; 274 T;

Query Match 35.7%; Score 267; DB 1; Length 1074;
Best Local Similarity 63.4%; Pred. No. 2.7e-65;
Matches 427; Conservative 0; Mismatches 240; Indels 6; Gaps 1;

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Db 535 AGGTTAGTGGCAGTGTGATCTGACAAAGATTATTCTCTACCACTTAGCACCTGGAGTAT 594
QY 247 GAAGACTTGCTGCTACGATTAATCTGACGAACGTTTAAATACCTCCGTTGATTCGAGAC 306
Db 595 GAAGATATGGAATTTATTTATTTGCTACAGATATGATGATTTCTTGACAGCTTCGAGGG 654
QY 307 GGTACCAAGGTGGAATTAACCTAGTGGCGGTGTGTTCTGTGTGCGGTGATCTGGT 366
Db 655 GGGACCAAGCTGGAATTAAC-----GGAGGGGGTGGGCTGGGGCGGTGGCGATGGGT 708
QY 367 GGTGGCGGTCTTCAGTCCAACTGTGCAATCCGGCGCGAGGTCAAGAACCGAGGGCC 426
Db 709 GGGGGGGGCTCTGAGGTTGACCTCCAGCATCTGGGACCTGTACTGGCAAGGCTGGGGCT 768
QY 427 TCAGTCAAGTGTCCCTTAAGCTACGGCTATATTTTCTATATGATGATTCATAGG 486
Db 769 TCAGTCAAGTGTCCCTTAAGGCTCTGGCTACACCTTTTCCAGTACGTGATGACCTGG 828
QY 487 GTGCTCAGGCCCGGCGGCGCTGGAATGATGAGTGTGATCTTACCGGCTCTGGT 546
Db 829 ATAAACAGAGGCGCTGACAGGCTGTGACCTGATGCTATGATCTCGAATTAAT 888
QY 547 AGCACCAGATATACGAAATTTTAAAGACCGTGTACTATGACGCGGTGACACTTGACT 606
Db 889 GATACATATTATCAACCCCAATTCACCAAGGCCAAACCTAGCTGACACTCCACCC 948
QY 607 AGTACAGTATACATGAGACTCTCCAGCTGCGATCGGAGAGACAGGCCCTATTATTCC 666
Db 949 AGCACTGCTACATGGAAGCTCAACAGCCTGACCAATGAGAGACTCTGCTTACTGT 1008
QY 667 GCGGCTATTATTT 679
Db 1009 ACCCCTTTATT 1021

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RESULT 15
T94968
ID T94968 standard; DNA; 1074 BP.
AC T94968;
DE 20-APR-1998 (first entry)
DE R. pipiens recombinant RNase ronc fusion protein 6 DNA.
KW RNase A; ribonuclease; cytotoxic; onconase; nonc; immunofusion;
KM tumour cell growth; frog; ss.
OS Rana pipiens.
OS Synthetic.
PN WO9731116-A2.
PD 28-AUG-1997.
PF 19-FEB-1997; U02588.
PR 21-FEB-1996; US-011800.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PI Bogue L, Newton DL, Rybak SM, Wlodawer A;
DR WPI; 97-435168/40.
DR P-PSDB; W35130.
PT Ribonuclease molecules based on native Onconase - used for killing
PT cells, particularly tumour cells.
PS Disclosure; Page 72; 90pp; English.
CC Sequences T94963 to T94973 encode recombinant fusion proteins (rOnc)
CC which are modifications of the RNase Onconase (RNM) (nonc). Such novel
CC ribonuclease molecules are highly cytotoxic and can be used alone or
CC to form chemical conjugates or to target recombinant immunofusions. They
CC are used particularly for decreasing tumour cell growth. They can also be
CC used for cell separation in vitro by selectively killing unwanted types
CC of cells, e.g. in bone marrow prior to transplantation into a patient
CC undergoing marrow ablation by radiation, or for killing leukaemia cells
CC or T-cells that would cause graft versus host disease. The toxins can
CC also be used to selectively kill unwanted cells in culture. The new
CC ribonucleases have increased cytotoxic activity compared to nonc and also
CC lower immunogenicity in humans.
SQ Sequence 1074 BP; 304 A; 244 C; 252 G; 274 T;

Query Match 35.7%; Score 267; DB 1; Length 1074;

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Best Local Similarity 63.4%; Pred. No. 2.7e-65;				Matches 427; Conservative 0; Mismatches 240; Indels 6; Gaps 1;			
Qy	7	GATATCCAGATGACCCAGTCCCGCTCCCTCCCTGTCGCGGATAGGGTCAACC	66				
Db	355	GACATCAAGATGACCCAGTCCCGCTCCCTCCCTGTCGCGGATAGGGTCAACC	414				
Qy	67	ATCACCTCGGCGGACGCAAAACATCTATGGCGGCTGAACCTGGTATCAACGTAAACCT	126				
Db	415	TTCACTTCAAGGCGAGTCAAGACATTAATACTATTATGCTGGTCCAGCAGAAACCA	474				
Qy	127	GGGAAGCTCCGAAGCTTCTGATTTACGGTGGCGAACCCTGGCAGATGAGTCCCTTCT	186				
Db	475	GGGAATCTCCTAAGACCTGATCTATCGTGCAACAGACTGGTAGTGGGTCCCATCA	534				
Qy	187	CGCTTCTCTGATCCGGTCCGGACGGAATTCATCTGACCATCAGCAGTCTGAGCCT	246				
Db	535	AGGTTCACTGGCAGTGGATCTGGCAAGATTAATCTCACCATAGCAGCTGGAGTAT	594				
Qy	247	GAAGACTTCGCTACGTATTACTGTGAGAACGTTTAAATACCTCCGTTGACTTCGGACAG	306				
Db	595	GAAGATATGGGATTTATTTATGTTCTACAGTATGATGATTTCCGTACAGTTCGGAGGG	654				
Qy	307	GGTACCAAGTGGAAATAAAGCTACTGGCGGTGGTGGTCTGGTGGCGGTGGATCTGGT	366				
Db	655	GGGACCAAGCTGGAATAAAA-----GGAGCGGTGGCTCGGCGGTGGCGGATCGGT	708				
Qy	367	GGTGGCGGTCTCAAGTCCAGTCCGCTGTCGAAATCCGCGCGGAGGTCAAGAAGCCAGGGCC	426				
Db	709	GGCGCGGCTCTGAGGTTCAAGTCCAGCAGTCTGGGACTGTACTGGCAAGGCTGGGGCT	768				
Qy	427	TCAGTCAAAGTCTCTGTAAGCTAGCGGCTATATTTTCTAATTATTGGATTCAATGG	486				
Db	769	TCAGTGAAGATGCTCTGCNAGGCTTCTGGCTACACCTTTCCAGCTACTGGATGCACGG	828				
Qy	487	GTGCGTCAAGCCCCCGGCGAGGCGCTGGAATGGATGGGTGAGATCTTACCGGCTCTGGT	546				
Db	829	ATAAAACAGAGGCGCTGGACAGGCTGCGACTGGATTGCTGCTATTGATCCTCGAAATAGT	888				
Qy	547	AGCACCGAATATACCGAAATTTTAAAGACCGTGTACTATGACGCGTGACACTTCGACT	606				
Db	889	GATACTATTTACACCCCGCAATTCAAACACAGGCGCAAACTGACTCAGTCACTCCACC	948				
Qy	607	AGTACAGTATACATGAGCTCTCCAGCTCGGATCGGAGGACACGCGCTCTATTATTGC	666				
Db	949	AGCATGCTCTACATGGAATCAACAGCTCAACAAATGAGGACTCTCGGCTATTACTGT	1008				
Qy	667	GGCGGTATTTTT	679				
Db	1009	ACCCCTCTTTATT	1021				

Search completed: September 12, 2000, 21:01:09
Job time: 3578 sec

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OM nucleic - nucleic search, using sw model

Run on: September 12, 2000, 19:20:03 ; Search time 56.72 Seconds
(without alignments)
1811.604 Million cell updates/sec

Title: US-08-487-283a-8
747
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Sequence:

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 243080 seqs, 68777915 residues

Total number of hits satisfying chosen parameters: 486160 *

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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3: /cgnl_7/ptodata/1/ina/5B_COMB.seq:*
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5: /cgnl_7/ptodata/1/ina/5D_COMB.seq:*
6: /cgnl_7/ptodata/1/ina/6_COMB.seq:*
7: /cgnl_7/ptodata/1/ina/PCrus_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	294	39.4	819	3	US-08-400-115-3
2	283.4	37.9	723	1	US-07-988-430-92
3	283.4	37.9	723	1	US-08-425-336-89
4	283.4	37.9	723	2	US-08-488-1138-89
5	283.4	37.9	723	2	US-08-477-4848-89
6	283.4	37.9	723	3	US-08-646-360-89
7	283.4	37.9	723	6	PCT-US92-09487-92
8	267	35.7	1065	5	US-08-875-811-40
9	267	35.7	1065	5	US-08-875-811-48
10	267	35.7	1074	5	US-08-875-811-44
11	267	35.7	1074	5	US-08-875-811-50
12	267	35.7	1086	5	US-08-875-811-46
13	267	35.7	1137	5	US-08-875-811-42
14	250	33.5	729	1	US-08-230-843-3
15	250	33.5	729	3	US-08-636-936-3
16	247.2	33.1	916	1	US-08-121-054C-29
17	236.6	31.7	733	4	US-08-224-591-17
18	236.6	31.7	733	4	US-08-926-789-17
19	234.4	31.4	721	3	US-08-224-591-15
20	234.4	31.4	721	4	US-08-926-789-15
21	232.4	31.1	2178	2	US-08-463-587A-24
22	232.4	31.1	2178	3	US-08-463-667A-2
23	232.4	31.1	2178	3	US-08-923-854-24
24	232.4	31.1	2178	6	PCT-US91-09133-25
25	231	30.9	6727	3	US-08-125-462-2
26	231	30.9	6727	4	US-08-891-848-2

27	230.6	30.9	1299	3	US-08-125-462-6	Sequence 6, Appl1
28	230.6	30.9	1299	4	US-08-891-848-6	Sequence 6, Appl1
29	230.6	30.9	1320	3	US-08-125-462-3	Sequence 3, Appl1
30	230.6	30.9	1320	4	US-08-891-848-3	Sequence 3, Appl1
31	230.6	30.9	6799	3	US-08-125-462-5	Sequence 5, Appl1
32	230.6	30.9	6799	4	US-08-891-848-5	Sequence 5, Appl1
33	224.4	30.0	732	1	US-08-230-843-1	Sequence 1, Appl1
34	224.4	30.0	732	1	US-08-636-936-1	Sequence 1, Appl1
35	223.2	29.9	6127	4	US-08-887-352B-1	Sequence 1, Appl1
36	221.8	29.7	720	1	US-08-061-092A-2	Sequence 2, Appl1
37	220.6	29.5	7305	1	US-08-286-740-4	Sequence 4, Appl1
38	220.6	29.5	7305	6	PCT-US93-09376-4	Sequence 4, Appl1
39	218	29.2	737	4	US-08-860-174A-1	Sequence 1, Appl1
40	216.2	28.9	1460	3	US-08-392-338A-18	Sequence 18, Appl1
41	216.2	28.9	1460	5	US-09-166-750-18	Sequence 18, Appl1
42	216.2	28.9	1460	5	US-09-166-093-18	Sequence 18, Appl1
43	215.8	28.9	797	2	US-08-323-445A-3	Sequence 3, Appl1
44	215.8	28.9	797	2	US-08-515-903A-3	Sequence 3, Appl1
45	215.8	28.9	797	6	PCT-US95-12840-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-08-400-115-3
Sequence 3, Application US/08400115
Patent No. 5864019
GENERAL INFORMATION:
APPLICANT: KING, David John
APPLICANT: MOUNTAIN, Andrew
APPLICANT: OWENS, Raymond John
APPLICANT: YARBANTON, Geoffrey Thomas
TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/400,115
FILING DATE: 06-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,136
FILING DATE: 27-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/842,193
FILING DATE: 17-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/00935
FILING DATE: 11-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9012995.8
FILING DATE: 11-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: ISACSON, John P.
REGISTRATION NUMBER: 33,715
REFERENCE/DOCKET NUMBER: 040283/0106 CARA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 819 base pairs
TYPE: nucleic acid

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; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..816
US-08-400-115-3

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Query Match	39.4%	Score 294;	DB 3;	Length 819;
Best Local Similarity	66.3%;	Pred. No. 2.6e-84;		
Matches 439;	Conservative 0;	Mismatches 220;	Indels 3;	Gaps 1;
QY	4	GCGGATATCCAGATGACCCAGTCCCGCTCCCTGCTGCCGCTCTGTGGGCGATAGGGTC	63	
DB	64	GCTGATATCCAGATGACTCAGTCTCCAGCCCTCCCTATCTGTATCTGTGGGAGAACTGTC	123	
QY	64	ACCATCACCTCGCGCGCCAGCGAAACATCTATGGCGGCTGAACTGTATCAACGTAAA	123	
DB	124	ACCATCACATGTCGAGCAATGAGCAATATTTACAGTAAATTTAGCATGTGTATCAACAGAA	183	
QY	124	CTTGGGAAAGCTCGAAGCTTCTGATTACGGTGGGAGAACCTGGCAGATGGAGTCCCT	183	
DB	184	CAGGGAAATCTCCTCAGCTCCTGGTCTATGCTGCAACAACTTAGCAGATGGTGTGCCA	243	
QY	184	TCCTGCTTCTGATCCGGCTCCGGACGATTTCACTCTGACCATCAGCAGTCTGCAG	243	
DB	244	TCAGGTTTCACTGAGTGGGACGTCGGGACACAGTATTCCTCAAGATCAACAGCTGCAG	303	
QY	244	CCTGAACACTTCGCTAGCTATTACTGTGCAGAACGTTTTAAATACTCCGTTGCATTTCCGA	303	
DB	304	TCGAAGATTTTGGGAGTTATTACTGTCAACATTTTGGGGTACTCCGTACACGTTCCGA	363	
QY	304	CAGGGTACCAAGTGGGAAATAAAGTACTGGCGGTGGTGTCTGTGGCGGTGGATCT	363	
DB	364	GGGGGACCAAGCTTGAAATAAAACG---TGTGGCGGGGATCCGGCGGGGAGGTTCA	420	
QY	364	GGTGTGGCGGTCTCAAGTCCAAGTGGTGAATCCGCGCGGAGGTCAAGAGCCAGGG	423	
DB	421	GGGGGTGGCGGATCCCAAGGTTACGCTCAGCAGTCTGACGTGAGTGGTGAACACTGG	480	
QY	424	GCCTCAGTCAAGTGTCTGTGAAAGCTAGCGGCTATATTTTCTTAATTTGGATTCAA	483	
DB	481	GCTTCAGTGAAGATATCTGCAAGGCTTCTGGCTACACCTTCATGACCATGCTATTAC	540	
QY	484	TGGTGGCTCAGGCCCCGGGCGAGGCGCTGGAATGGATGGGTGAGATCTTACCGGGCTCT	543	
DB	541	TGGCGAAGCAGAAGCTGAACAGGCGCTGGAATGGATTGGATATATTTCTCCCGGAAAT	600	
QY	544	GGTAGCACCGNATATACGGAATAATTTAAAGACCGTGTACTATGACCGGTGACACTTCG	603	
DB	601	GATGATATTAAAGTACAATGAGAAGTTCAAGGGCAAGGCCACACTGACTGCAGACAAATCC	660	
QY	604	ACTAGTACAGTATACATGGAGCTCTCCAAGCTCGCATCGGAGGACACGGCGTCTATTAT	663	
DB	661	TCCAGCACTGCCATACATGCAGCTCAACAGCCTGACATCTGAGGATTTGCAAGTGTATTTC	720	
QY	664	TG	665	
DB	721	TG	722	

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RESULT      2
US-07-988-430-92
; Sequence 92, Application US/07988430
; Patent No. 5416202
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Lane, Julie A.
; APPLICANT: Lei, Shau-Ping
; TITLE OF INVENTION: Materials Comprising and Methods of
; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins

```

NUMBER OF SEQUENCES: 101
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ADDRESSEE: Bicknell
 STREET: Two First National Plaza, 20 South Clark
 STREET: Street
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60603
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/988,430
 FILING DATE: 19921209
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/901,707
 FILING DATE: 19-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/787,567
 FILING DATE: 04-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: NO. 5416202and, Greta E.
 REGISTRATION NUMBER: 35302
 REFERENCE/DOCKET NUMBER: 31133
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 346-5750
 TELEFAX: (312) 984-9740
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 92:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 723 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 US-07-988-430-92

Query Match	37.9%; Score 283.4; DB 1; Length 723;
Best Local Similarity	63.7%; Pred. No. 5.8e-81;
Matches	472; Conservative 0; Mismatches 251; Indels 18; Gaps 2;
Qy 7	GATATCCAGATGACCCAGTCCCGGTCTCCCTGTCCGCTCTGTGGCGATAGGGTCAACC 66
Db 1	GACATCCAGATGACTAGCTCCCATCTCCCTGTCTGCATCTGTAGGACAGAGTCACT 60
Qy 67	ATCACTCGCGCGCAGCGAAACATCTATGGCGGCTGAACTGTATCAACGTAAACCT 126
Db 61	ATCACTGCCGGCGATCAGGACATTAATAGCTATTTAGCTGGTCCACGACGAACCA 120
Qy 127	GGGAAGCTCCGAAGCTTCTGATTACGGTCCGACGACCTGGCAGATGGAGTCCCTTCT 186
Db 121	GGAAAGCTCTAAGACCCCTGATCTATCGTCAAAACAGATTGGAATCTGGGGTCCCATCA 180
Qy 187	CGTCTCTCTGATCCGGTCCGGACGGAATTTACTCTGACCATCAGCAGTCTCGAGCCT 246
Db 181	AGGTTCACTGGCAGTGGATCTGGGACAGATTATACTCTCACCATCAGCAGCCTGCAATAT 240
Qy 247	GAAGACTTCGCTACGTATTACTGTCAAGACGTTTAAATATCCGTTGACATTTGGACAG 306
Db 241	GAAGATTTTGGAAATTAATATGTCAACAGTATGATGAGTCTCGGTGGACCTCGGTGGA 300
Qy 307	GGTACCAAGGTGGAAATAAAACGTACTGGCGGTGGTGGTTCTGGTGGCGGTGGATCTGGT 366
Db 301	GGACCAAGCTTGAGATGAAA-----GGTGGCGGTGGATCTGGTGGAGGTGGGTCCGGA 354
Qy 367	GGTGGCGGTTCTCAAGTCCAACTGGTGCAATCCGCGCGCGAGGTCAAGAACCCAGGGGCC 426

11

Db 355 GGTGGAGGATCTGAGATCCAGTTGGTCTGAGAGAGCCCTGGTGAAGCTGGAGGG 414
Oy 427 TCAGTCAAACTGCTCTGTAAGAGTACGGCTATATTTTCTAATTAATTTGATTCATGG 486
Db 415 TCCGTAGGATCTCTCGAGAGCTTCCTGGGATACCTTCACAACTATGGAATGACTGG 474
Oy 487 GTCCGTGAGCCCCCGGAGAGCCCTGGAAATGATGGGTGATCTTAACGGGCTGTGGT 546
Db 475 GTCCGCGAGCTCCAGGAAAGGTTTAGAGTGATGGCTGATTAACACACACACTGGA 534
Oy 547 AGACCGGAATATCCGAAATTTTAAGACCCGTCTTACTATGAGCGCGAATCTCGACT 606
Db 535 GACCCACATATCTGATCTTCTTCAAGGAGGTTTACCTTCTTGGAGATCTTAG 594
Oy 607 AGTACAGTATACAGAGCTCTCCAGCTCGATCGAGAGACAGCGCGCTTATTATTC 666
Db 595 AACACGCGCTATTTACGATCAGACAGCTTCAGACCGAGGACGCGCTGTATTTCTGT 654
Oy 667 GCGCGTATTTTGTGTTCTAGCCGAATTTGATTTTGTGTTGGGTCAAGGAACC 726
Db 655 ACAAGACGGGGTTACG-----ACTGTAATTCGATGTCTGGGCGCAAGGAGAC 702
Oy 727 CTGCTACTGTCTCGAGCTGA 747
Db 703 ACGGTACCGCTCTCTCATGA 723

RESULT 3
US-08-425-336-89
Sequence 89, Application US/08425336
Patent No. 5621083
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,336
FILING DATE: 18-APR-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Thomas C.
REGISTRATION NUMBER: P-36,989
REFERENCE/DOCKET NUMBER: 31394
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEO ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-425-336-89

Query Match 37.9%; Score 283.4; DB 1; Length 723;
Best Local Similarity 63.7%; Pred. No. 5.8e-81;
Matches 472; Conservative 0; Mismatches 251; Indels 18; Gaps 2;

Oy 7 GATATCAGATGACCAGTCCCGCTCCCTGCTCCCTGCTGCTGAGGCGATAGGCTACC 66
Db 1 GACATCCAGATGACTACGATCCATCTTCCCTGCTGCTGATCTGTAGAGACAGAGTCACT 60
Oy 67 ATCACTGCGGCGCCAGAGGAAACATCTATGGCGCGCTGAACTGTATCAAGTAACT 126
Db 61 ATCACTTCCCGGCGAGTCAAGACATTAATACCTTTTAAAGCTGGTTCAGAGGAACCA 120
Oy 127 GGAAGAGTCCGAACTCTGATTAAGGTGCGAGAACCTGGCAGATGGAGTCCCTCT 186
Db 121 GGAAGAGTCCCTAAGACCTGATCTATGCTGCAACAGATTGGAATCTGGGCTCCATCA 180
Oy 187 CGCTCTCTGATCCGCTCCGGAAGGATTTCACTCTGACCATGACAGTCTGAGCCT 246
Db 181 AGGTCAAGTGGCAGTGAATCTGGGACAGATTTATCTTCACCATCAGACGCTGCATAT 240
Oy 247 GAAGATTCGCTACGTATTTACTGTGAGAACGTTTAAATACTCCGTTGACCTTGGACAG 306
Db 241 GAAGATTTTGGAAATTAATTAATTTGTCACAGTATGATGATGATCCGCTGACGTTTGGTGA 300
Oy 307 GGTACCAAGTGGGAATTAACGCTACTGGCGGTGGTGGTCTGGTGGCGGTGGATCTGT 366
Db 301 GGCACCAAGCTTGAGATGA-----GGTGGGTGATCTGGTGGAGGTGGTCCGA 354
Oy 367 GTGGCGGTTTCAAGTCCAACTGTCGATCCGCGCGGAGTCAAGAACGACGAGGCC 426
Db 355 GGTGAGGATCTGAGATCAGATGAGTGTGAGTGTGAGGAGGCCCTGTGAAGCTTGAGGG 414
Oy 427 TCAGTCAAAAGTGTCTGTAAAGCTAGCGGCTATATTTTCTAATTAATTTGATTCATGG 486
Db 415 TCCGTCAAAATCTCCTCGGACGCTTCTGGTATCTTCAAACTATGGAATGAATCT 474
Oy 487 GTGGTCAAGGCCCCCGGAGAGGCGCTGGAATGAGGTGAGATCTTACCGGCTCTGT 546
Db 475 GTGGCGGAGGCTCCAGGAAAGGTTTAAAGTGAAGGCTGCTGATAACACCCCACTGGA 534
Oy 547 AGACCGGAATATCCGAAATTTTAAGACCGTGTACTATGACCGTGAACCTTCGACT 606
Db 535 GAGCCACATATGCTGATCTTTTCAAGGAGCGTTTACTCTCTTTGGACATTTCTAAG 594
Oy 607 AGTACAGTATACAGAGCTCTCCAGCTCGATCGAGAGACAGCGCGCTCTATTATTC 666
Db 595 AACACTGCTATTTACAGATCAAGAGCTTCAGAGCGGAGACGCGCTGTATTTCTGT 654
Oy 667 GCGCGTATTTTGTGTTCTAGCCGAATTTGATTTTGTGTTGGGTCAAGGAACC 726
Db 655 ACAAGACGGGGTTACG-----ACTGTAATTCGATGTCTGGGCGCAAGGAGAC 702
Oy 727 CTGCTACTGTCTCGAGCTGA 747
Db 703 ACGGTACCGCTCTCTCATGA 723

RESULT 4
US-08-488-1138-89
Sequence 89, Application US/084881138
Patent No. 5744580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating


```

1  TITLE OF INVENTION:  Proteins
2  NUMBER OF SEQUENCES:  169
3  CORRESPONDENCE ADDRESS:
4  ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
5  STREET:  500 West Madison Street, 34th floor
6  CITY:  Chicago
7  STATE:  Illinois
8  COUNTRY:  USA
9  ZIP:  60661
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE:  Floppy disk
12 COMPUTER:  IBM PC compatible
13 OPERATING SYSTEM:  PC-DOS/MS-DOS
14 SOFTWARE:  PatentIn Release #1.0, Version #1.25
15 CURRENT APPLICATION DATA:
16 APPLICATION NUMBER:  US/08/488,113B
17 FILING DATE:  07-JUN-1995
18 CLASSIFICATION:  530
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER:  US 08/425,336
21 FILING DATE:  18-APR-1995
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER:  US 08/064,691
24 FILING DATE:  12-MAY-1993
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER:  US 07/988,430
27 FILING DATE:  09-DEC-1992
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER:  US 07/901,707
30 FILING DATE:  19-JUN-1992
31 PRIOR APPLICATION DATA:
32 APPLICATION NUMBER:  US 07/787,567
33 FILING DATE:  04-NOV-1991
34 ATTORNEY/AGENT INFORMATION:
35 NAME:  McNicholas, Janet M.
36 REGISTRATION NUMBER:  32,918
37 REFERENCE/DOCKET NUMBER:  11022US07/200-70.P3.C
38 TELECOMMUNICATION INFORMATION:
39 TELEPHONE:  312/707-8889
40 TELEFAX:  312/707-9155
41 TELEX:  650 388-1248
42 INFORMATION FOR SEQ ID NO:  89:
43 SEQUENCE CHARACTERISTICS:
44 LENGTH:  723 base pairs
45 TYPE:  nucleic acid
46 STRANDEDNESS:  single
47 TOPOLOGY:  linear
48 MOLECULE TYPE:  DNA
49 US-08-488-113B-89

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[illegible]

Db	241	GAGATTTTGGAAATTTATTTATGTCACACAGTATGATGAGTCTCCGTGGAGACGTTTCGGTGGA	300
QY	307	GGTACCAAGGTGGAAATAAAACACTACTGGCGGTGSGTGTCTTGGTGGCGGTGSGATCTGCT	366
Db	301	GGCACCAGCTTGAGATGAAA-----GGTGGCGGTGGATCTGGTGGAGTGGGTCCGGA	354
QY	367	GGTGGCGGTTCTCAAGTCCAACTGGTGGCAATCCGGCGCGGAGGTCAAGAAGCCAGGGGCC	426
Db	355	GGTGGAGGATCTGAGATCCAGTTGGTGCAGTCTGGAGAGAGGCGCTGGTGAAGCTTGAGGG	414
QY	427	TCAGTCAAGATGTCCTCTAAAGCTAGCGGCTATATTTTTTCTTAATTTATTTGGATTCAATCG	486
Db	415	TCGGTCAAGATCTCCCTGCGCAGCTTCTGGGTATACCTTCACAACTATGGAATGAACTGG	474
QY	487	GTGGCTCAGCGCCCGGGCAGGCGCTGGAATGGATGGGTGAGATCTTACC GGCGCTCTGGT	546
Db	475	GTGGCCAGGCTCCAGGAAGGTTTAGAGTGGATGGCTGGATAAACACCCACACTGGA	534
QY	547	AGCACCGAATATACCGAAAATTTTAAAGACCGGTGTACTATGACGGTGACACTTCGACT	606
Db	535	GAGCCAAACATATGCTGATCTTTCAAGGGACGGTTTACCTTCTCTTTGGACGATTCTAAG	594
QY	607	AGTACAGTATACATGGAGCTCTCCAGCCTCGATCGGAGACACAGCGCTCTATTTATTCG	666
Db	595	AACACTGCCATTATTACAGATCAACAGCCTCAGAGCCGAGGACACGGCTGTGTAATTTCT	654
QY	667	CGCGGTTATTTTTTGGTCTTAGCCCGAAATGGTATTTTATGCTTTGGGTCAAGGAACC	726
Db	655	ACAGACGGGTACG-----ACGTGACTTCGATCTCTGGGCCAAGGGACC	702
QY	727	CTGCTCACTGTCGAGCTGA	747
Db	703	ACGGTCACCGCTCCTCATGA	723
RESULT 5			
US-08-477-484B-89			
; Sequence 89, Application US/08477484B			
; Patent No. 5755699			
; GENERAL INFORMATION:			
; APPLICANT: Better, Marc D.			
; APPLICANT: Carroll, Stephen F.			
; APPLICANT: Studnika, Gary M.			
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating			
; TITLE OF INVENTION: Proteins			
; NUMBER OF SEQUENCES: 169			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.			
; STREET: 500 West Madison Street, 34th floor			
; CITY: Chicago			
; STATE: Illinois			
; COUNTRY: USA			
; ZIP: 60661			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.25			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/477,484B			
; FILING DATE: 07-JUN-1995			
; CLASSIFICATION: 530			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 08/425,336			
; FILING DATE: 18-APR-1995			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 08/064,691			
; FILING DATE: 12-MAY-1993			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 07/988,430			
; FILING DATE: 09-DEC-1992			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 07/901,707			

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? FILING DATE: 19-JUN-1992
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/787,567
? FILING DATE: 04-NOV-1991
? ATTORNEY/AGENT INFORMATION:
? NAME: McNicholas, Janet M.
? REGISTRATION NUMBER: 32,918
? REFERENCE/DOCKET NUMBER: 110220US07/200-70.P3.C2A
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 312/707-8889
? TELEFAX: 312/707-9155
? TELE: 650 388-1248
? INFORMATION FOR SEQ ID NO: 89:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 723 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: DNA
? US-08-477-484B-89

```

Query Match	37.9%	Score 283.4	DB 2	Length 723
Best Local Similarity	63.7%	Pred. No. 5.8e-81		
Matches 472; Conservative	0	Mismatches 251	Indels 18	Gaps 2

QY	/	GATATCCAGATGACCACGATCCCGCTCTCCCTGTGACCGCCCTCTGTGGGCGATAGGCTACC	66
Db	1	GACATCCAGATGACTCATGCTCCATCTCCCTCTGTGCATCTGTAGAGACAGAGTCACT	60
QY	67	ATCACCTCGGGCGCCACGAGAAAACATCTATGCGCGCTGAACTGATATCAAGTAAACCT	126
Db	61	ATCACTTGGCCGGGAGAGCAGACATTAAATGATTAATTAAGCTGTGTTCCAGCAGAAACCA	120
QY	127	GGGAAAGCTCCGAGACTTCTGATTACGGTGCAGACGAACTGGCAGATGGAGTCCCTTCT	186
Db	121	GGGAAAGCTCTATAGACCCCTGATCTATCGTGCACAAACGATTGGAAATGGGGTCCATCA	180
QY	187	CGCTTCTCTGGATCCGCGCTCCGAGCGAATTTCACTGTGACCATCAGACAGTTCGACCT	246
Db	181	AGGTTTCAGTGCAGATGGATCTGGGACAGATATATCTCTCACAATCAGACACCTGCAATAT	240
QY	247	GAACACTTCGCTAGCTATTAATCTACCAAGCTTTAAATACCTCGTACGATTTTTCGGACG	306
Db	241	GAAATTTTGGAAATTTTATTTATGTCCAACAGTATATGATAGTCTCCGTGGAAGTTTCGGGGA	300
QY	307	GGTACCAAGAGTGAAATAAACGCTACTGCGGCGTGGTCTGGTGCAGGTGATCTGAT	366
Db	301	GGCACCAAGCTTGGATGAGAA-----GGTGGCGGTGATCTGGTGGAGGTGGGCTCCGA	354
QY	367	GGTGGCGGTTTCAAGTCCAACTGCTGTCATCCGGCGCCGACAGTCAAGAAACCAAGGGCC	426
Db	355	GGTGGAGGATCTGGAGATCCAACTTGTCAGACTGTGAGAGAGCCCTGGAGACCTTGAGGG	414
QY	427	TCACTCAAAGTGTCTCTGTAAGAGTACGAGCGCTATATTTTCTTAATTTATGATTCATG	486
Db	415	TCCGTCAGAAATCTCTCGCGCAGCTTCTGGGATATACCTTTCACAAACTATGGAATGAAGTGG	474
QY	487	GTCGCTAGCGCCCCCGGACAGGCGCTGGAATGATGGGTAGATCTTACCGGGGCTCTGT	546
Db	475	GTCGGCCAGGCTCCAGAGAAAGGGTTTAGAGATGGCTGAGATAAACACCCACACTCGA	534
QY	547	AGCACCGAATTTACCGGAAATTTTAAAGACCGCTGTACTATGACCGCTGACACTTGACT	606
Db	535	GAGCCACAACTATGCTGATTTCTTTAABGGAGCGTTTACCTCTCTTTTGGACGATTTCAAG	594
QY	607	AGTACAGTATACATGAGAGCTCTCCAGCGCTGGATCGGAGACAGCGCGCTATATTATGC	666
Db	595	AACACTGCTATTTACAGATCAACAGCCTCAGACCGGAGACAGCGCTGTGTAATTCTGT	654
QY	667	GGCGGTAATTTTGGGTCTAGCCGCAATTTGTAATTTGATGTTTGGGTCAAAGAAC	726
Db	655	ACAAGACGGGGTTACG-----ACGTGACTCTCATATGCTCTGTGGGCGCAAGGAC	702

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QY      727 CTGGTCACTGTCTCGAGCTGA 747
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Db      703 ACGGTACCGTCTCCTCATGA 723

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RESULT 6
US-08-646-

; Sequence 89, Application US/086463360
; Patent No. 5837491
; GENERAL INFORMATION:

GENERAL INFORMATION: Marc D. Better, Applicant;
Applicant: Carrol, Stephen F.
Applicant: Studnka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
PROTEINS
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
PROTEINS
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:

```

: COMPUTER READABLE FORM:
:
: MEDIUM TYPE: Floppy disk
:
: COMPUTER: IBM PC compatible
:
: OPERATING SYSTEM: PC-DOS/MS-DOS
:
: SOFTWARE: PatentIn Release #1.0, Version #1.25
:
: COMPANY: PatentIn, Inc.

```

; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/646,360
 ; FILING DATE: 13-MAY-1996
 ; CLASSIFICATION: 530

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 10 MAR 1994

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;; FILING DATE: 12-MAY-1994
;; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064 691

APPLICATION NUMBER: 03 06/004, 05
 FILING DATE: 12-MAY-1993
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992

;; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707

;
; FILING DATE: 19-JUN-1992
;
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991

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;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: McNicholas, Janet M.
;
; REGISTRATION NUMBER: 33 919

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REGISTRATION NUMBER: 32,516
REFERENCE/DOCKET NUMBER: 200-70.F
TELECOMMUNICATION INFORMATION:

QY 7 GATATCCAGATGACCCAGTCCCCTCCTCCCTGTCCGGCTCTGTGGCGCATAGGGTCACC 66
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Db 1 GACATCCAGATGACTCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGAGACAGAGTCACT 60

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QY 67 ATCACTCGCGCCGAGCAAAACATCTATGGCGGCTGAACCTGGTATCAACGTAACCT 126
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Db 61 ATCACTTGGCGGAGTCAGGACATTAATAGCTATTTAAGCTGGTCCAGCAGAAACA 120

QY 127 GGGAAAGCTCGAAGCTTCTGATTAGCGTGGCAGCAACCTGGCAGATGGAGTCCCTTCT 186
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Db 121 GGGAAAGCTCTAAGACCTGATCTATCGTGCAACAGATTGGAATCTGGGTCCCATCA 180

QY 187 CGCTTCTCGATCCGCTCCGGAACGATTTCACTCTGACCATCAGCAGTTCGAGCT 246
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QY 307 GGTACCAAGTGGAAATTAACAGTACTGCGGTGGTGGTCTGCGGTGGGATCTGGT 366
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Db 301 GGCACCAAGCTTGAGATGAAA-----GGTGGCGGTGGATCTGGTGGAGGTGGGTCCGGA 354

QY 367 GGTGGCGGTTCCTCAAGTCCAACTGGTGCAATCCGCGCGGAGGTCAAGAACGAGGGCC 426
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Db 355 GGTGGAGGATCTGAGATCCAGTCTGGTGACGCTCGGAGGAGGCTGGTGAAGCTGGAGG 414

QY 427 TCAGTCAAAAGTGTCTGTAAAGCTAGCGGCTATATTTTTTCTAATTTATTTGATTCATGG 486
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Db 415 TCGCTCAGAATCTCTCGCAGCTTCTGGGTATACCTTCACAAACTATGGAATGAAGTGG 474

QY 487 GTGCGTACGCCCCCGGCGAGGCTGGATGGATGGGTGAGATCTTACCGGCTCTGGT 546
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Db 475 GTGCGCAGGCTCCAGGAAAGGTTTTAGAGTGGATGGGTGGATAAACACCCACACTGGA 534

QY 547 AGCACCGAATATACCCGAAATTTTAAAGACCGGTGTATGATGACGCTGACACTTCGACT 606
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Db 535 GAGCAACATATGCTGATTTCTTCAAGGAGCGGTTTACCTTCTTTTGGACGATCTAAG 594

QY 607 AGTACGATATACATGGAGCTCTCCAGCTCGATCGGATCGGAGGACGCGCTCTATTATTC 666
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Db 595 AACACTGCTATTACAGATCAACAGCTCAGAGCGGAGGACGCGCTGTGTATTCTTCTGT 654

QY 667 GCGGCTATTTTTTGGTCTAGCCGGAATTTGGTATTTTGGTGTGGGTCAAGGAACC 726
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Db 655 ACAAGACGGGTACG-----ACTGGTACTTCGATGCTGGGCGCAAGGGACC 702

QY 727 CTGCTACTGCTCGAGCTGA 747
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Db 703 ACGGTCACCGTCTCTCATGA 723

RESULT 7
PCT-US92-09487-92
; Sequence 92, Application PC/TUS9209487
; GENERAL INFORMATION:
; APPLICANT: Bernhardt, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroil, Stephen F.
; APPLICANT: Lane, Julie A.
; APPLICANT: Lei, Shau-Ping
; TITLE OF INVENTION: Materials Comprising and Methods of
; PREPARATION AND USE FOR RIBOSOME-INACTIVATING PROTEINS
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09487
; FILING DATE: 19921104
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35302
; REFERENCE/DOCKET NUMBER: 31133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 723 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; PCT-US92-09487-92
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Query Match 37.9%; Score 283.4; DB 6; Length 723;
Best Local Similarity 63.7%; Pred. No. 5.8e-81;
Matches 472; Conservative 0; Mismatches 251; Indels 18; Gaps 2;

QY 7 GATATCCAGATGACCCAGTCCCGCTCTCCCTCTGTCGCGCTCTGTCGGCGCATAGGGTCACC 66
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Db 1 GATATCCAGATGACCTCAGTCTCCATCTTCCCTCTGTCGATCTGTAGAGACAGTCACT 60

QY 67 ATCACTCGCGGCGCAGCGAAACATCTATGGCGGCTGAACCTGGTATCAACATAACCT 126
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QY 127 GGGAAAGCTTCGAGCTTCTGATTTACGCTGGCAGCAACCTGCGACATGGAGTCCCTTCT 186
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Db 121 GGGAAAGCTTCTAAGACCTGATCTATCTGTCACACAGATTGGAATCTGGGGTCCCATCA 180

QY 187 CGCTTCTCTGGATCCGCTCCGGAACGATTTTCACTCTGACCATCAGCAGTCTGCAAGCT 246
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QY 247 GAAGACTTCGCTACGCTATTTACTGTCTAGAACGTTTTTAAATCTCCGTGACTTTTCGACAG 306
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Db 241 GAAGATTTTGGATTTTATTTGTCACAGTATGATGAGTCTCCGTGGACGTTCCGGTGA 300

QY 307 GGTACCAAGTGGAAATTAACAGTACTGCGGTGGTGGTCTGCGGTGGGATCTGGTGGAG 366
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Db 301 GGCACCAAGCTTGAGATGAAA-----GGTGGCGGTGGATCTGGTGGAGGTGGGTCCGGA 354

QY 367 GGTGGCGGTTCCTCAAGTCCAACTGGTGCAATCCGCGCGGAGGTCAAGAACGAGGGCC 426
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Db 355 GGTGGAGGATCTGAGATCCAGTCTGGTGACGCTCGGAGGAGGCTGGTGAAGCTGGAGG 414

QY 427 TCAGTCAAAAGTGTCTGTAAAGCTAGCGGCTATATTTTTTCTAATTTATTTGATTCATGG 486
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Db 415 TCGCTCAGAATCTCTCGCAGCTTCTGGGTATACCTTCACAAACTATGGAATGAAGTGG 474

QY 487 GTGCGTACGCCCCCGGCGAGGCTGGATGGATGGGTGAGATCTTACCGGCTCTGGT 546
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Db 475 GTGCGCAGGCTCCAGGAAAGGTTTTAGAGTGGATGGGTGGATAAACACCCACACTGGA 534

QY 547 AGCACCGAATATACCCGAAATTTTAAAGACCGGTGTATGATGACGCTGACACTTCGACT 606
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Db 535 GAGCAACATATGCTGATCTTTCAAGGAGCGTTACCTTCTTTGGACATTTCTAAG 594
QY 607 AGTACAGTATACATGAGAGCTCTCCAGCCTGCATGAGAGACGCGCTTATTATTGC 666
Db 595 AACACTGCTATTACATCAAGATCAAGCCTCAGAGCGGAGACAGCGCTGTATTTCGT 654
QY 667 GCGCGTATTTTGTGTTCTAGCCCAATTGCTTTTGTATGTTGGGGTCAAGAAC 726
Db 655 ACAAGAGCGGGTACG-----ACTGTACTTCGATGCTGGGCGCAAGGAGACC 702
QY 727 CTGCTCACTGCTCGAGCTGA 747
Db 703 ACGGTACCGCTCTCCTCATGA 723

RESULT 8
US-08-875-811-40
Sequence 40, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Luis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 1065 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1065
OTHER INFORMATION: /note="sfvBmetGlunc"
US-08-875-811-40

Query Match 35.7%; Score 267; DB 5; Length 1065;
Best Local Similarity 63.4%; Pred. No. 1,2e-75;
Matches 427; Conservative 0; Mismatches 240; Indels 6; Gaps 1;

QY 7 GATATCCAGATGACCCAGTCCCGCTCCCTGTCGCGCTCTGTGGCGATAGGTACCC 66
Db 1 GACATCAAGATGACCCAGTCCCGCTCCCTGTCGCGCTCTGTGGCGATAGGTACCC 60
QY 67 ATCACTGGGGGCCGACGAAACATCTATGGGGCCCTGACCTGATGATCAAGTAACCT 126
Db 61 TTCACCTTGGAAGCGGAGTGAAGACATTAATTAATTAATTAATTAATTAATTAATTA 120
QY 127 GGGAAAGCTCCGAAGCTTGTATTTACGGTGGAGCAGACACAGTGGAGTGGAGTCCCT 186
Db 121 GGGAAATCTCTTAAGACCTGATCTTTCGTCAAAACAGACTGATGATGGGGTCCCATCA 180
QY 187 CGCTTCTGATATCCGCTCCGAGAGATTCCTGTCGACATCAATCAAGTCAAGTCCCT 246
Db 181 AGGTTCAGTGGAGTGGATCTGACAAAGATTAATCTCTCAGCATTTAGCAGCTCGAGTAT 240
QY 247 GAAGACTTGGCTATGATTTACTGTCAGAACGTTTAAATTAATTAATTAATTAATTA 306
Db 241 GAAGATATGGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 300
QY 307 GGTACCAAGTGGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 366
Db 301 GGTACCAAGTGGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 354
QY 367 GGTGGGCTTCTCAAGTCCAGTGTGCAATCCGCGCGCGAGTCAAGAACGCGAGGGCC 426
Db 355 GGTGGGCTTCTCAAGTGTGCAATCCGCGCGCGAGTCAAGAACGCGAGGGCC 414
QY 427 TCAGTCAAAAGTCTCTGTAAGCTAGCGGCTATATTTTCTAATTAATTAATTAATTA 486
Db 415 TCAGTCAAAAGTCTCTGTAAGCTAGCGGCTATATTTTCTAATTAATTAATTAATTA 474
QY 487 GTGCGTACGCCCCCGGAGGAGGCTGGAATGATGAGTGGATCTTACCGGGCTGTGT 546
Db 475 ATAAACAGAGGCTGGAAGGCTGGAATGATGAGTGGATCTTACCGGGCTGTGT 534
QY 547 AGCAGCAATATACGAAATTTTAAGACCGGTACTAGCGGGTGCACACTGACT 606
Db 535 GATCACTATTACACCCGCAATTCACACAGCCAACTGACTGACTGACTGACTGACT 594
QY 607 AGTACAGTATACATGAGGCTCTCCAGCTGCGATCGGAGACAGCGCGCTATTATTTC 666
Db 595 AGCACTGCTACATGAGACTCAACAGCCTGACAAATGAGAGACTCTCGGCTATTACTGT 654
QY 667 GCGCGTATTTT 679
Db 655 ACCCCTCTTATT 667

RESULT 9
US-08-875-811-48
Sequence 48, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Luis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:


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Db 415 TTCACTTCGAAGCGCAGTCAGGACATTAATACTATTATGCTGGTTCAGCAAGAACCA 474
QY 127 GGGAAAGCTCCGAAGCTTCTGATTTACGTCGGACGAACCTGGACAGATGAGATCCCTTCT 186
Db 475 GGGAAATCTCCTAAGACCTCTGATCTATGCTGCAAAACAGCTGTAGATGGGTCCTATCA 534
QY 187 CGCTTCTGATCCGGCTCCGGAACGATTTCACTGTGACCATGACAGCTGACGCT 246
Db 535 AGGTCACTGAGTGAAGTCTGCAACAGATTAATCTTCCATCATGACAGCTGGAGTAT 594
QY 247 GAAGCTTCGCTACATTTACTGTGACAGCTTTAAATACCTCCGTTGCTTGGACAG 306
Db 595 GAAGTAAAGGAAATTAATATGTTACAGTATGAGTATCCGTAACGTTCCGAGAGG 654
QY 307 GGTACCAAGGTGGAATATAAAGCTACTGGCGGTGGTGGTGGTGGTGGTGGTGGTGGT 366
Db 655 GGGACCAAGCTGGAATATAA-----GGAGCGGTGGTGGTGGTGGTGGTGGTGGTGGT 708
QY 367 GGTGGCGGTCTCAAGTCCAACTGGTGAATCGGCGCGGAGGTCAAGAACCGAGGGCC 426
Db 709 GCGCGCGCTCTGAGATTCAGCTCCAGCAAGTCTGGGACTGTACTGGCAAGGCTGGGGCT 768
QY 427 TCAGTCAAGTGTCTCTGTAAGCTAGCGGCTATATTTTCTTAATTATTGATTCATGG 486
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QY 487 GTGGCTGAGCGCCCGGCGAGGCGCTGGAATGATGGTGAATCTTACCGGCTCTGT 546
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QY 547 AGCAACCGAATATACCGAAATTTTAAAGCCGTGTACTATGACCGGTGACACTTGCAGT 606
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QY 607 AGTACATATACAGTGAAGCTCTCCAGCCTGCGATCGGAGACAGCGCGCTATATTATTC 666
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QY 667 GCGGCTTATTTT 679
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RESULT 11
US-08-875-811-50
; Sequence 50, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Luis
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588

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; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1074 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1074
; OTHER INFORMATION: /note="MetGluonCFB6"
US-08-875-811-50

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Query Match 35.7%; Score 267; DB 5; Length 1074;

Best Local Similarity 63.4%; Pred. No. 1.2e-75; Matches 427; Conservative 0; Mismatches 240; Indels 6; Gaps 1;

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QY 7 GATATCCAGATGACCCAGTCCCGTCCCTCCGCTCTGTCGGCGATAGGATCACC 66
Db 355 GATACATAAGATGACCCAGTCCCGTCCCTCCGCTCTGTCGGCGATAGGATCACC 414
QY 67 ATACCTGCGGCGCCAGCCGAAACATCTATGGCGCGCTGACCTGATCTCAAGTAACT 126
Db 415 TTCACTTCCAGGCGAGTCAAGCAATTAATTAATTAATTAATTAATTAATTAATTA 474
QY 127 GGGAAAGCTCCGAAGTGTGATTTACGTCGAGCAGCAACTGGACAGTGGATGCCCTTC 186
Db 475 GGGAAATCTCTTAAGACCCCTGATCTATCGTCAACAGACTGTGATGGATGCCCTTC 354
QY 187 CGCTCTCTGATCCGCTCCGAGCGATTTCACTGTGACATCAAGCACTGACGCT 246
Db 535 AGGTTCAGTGGCAGTGTGATGCAAGATTAATCTCTACCACTTACAGCTGGAGTAT 594
QY 247 GAAGACTTGGCTACATTAAGTCTCAGAACGTTTAAATATCCGTTGACTTTCGACAG 306
Db 595 GAAGATATGGATTTATTTATTTCTACAGTATGATGATGATGATGATGATGATGATG 654
QY 307 GGTACCAAGGTGGAATTAATAAGCTACTGGGCGTGGTGTCTGTGGCGGTGGATCTGT 366
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QY 367 GGTGGCGGTCTCAAGTCCAACTGTGCAATCCGCGCGCAGGTCAAAGAACAGGGGCC 426
Db 709 GCGCGCGCTCTAAGTTCAAGTCTCAGCACTCTGGGACTTATGCGCAAGCCCTGGGCT 768
QY 427 TCAGTCAAGTGTCTCTGTAAGCTAGCGGCTATATTTTCTTAATTATTGATTCATGG 486
Db 769 TCAGTGAAGTGTCTCTGCAAGGCTTCTGCTACACCTTTCCAGCTACTGATGAC 828
QY 487 GTGCGTCAAGGCGCCCGGCGAGGCGCTGGAATGATGGTGAATCTTACCGGCTCTGT 546
Db 829 ATAAACAGAGGCTGAGAGGCTGTGAGTGTGCTATGCTATGATCTCGAAATATG 888
QY 547 AGACCGAATATACCGAAATTTTAAAGCCGTGTACTATGACGCTGACATCTGAC 606
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QY 607 AGTACATATACATGAGCTCTCAGCTGCGATCGGAGACAGCGCGCTATATTATTC 666
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QY 667 GCGGTTATTTT 679
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Db 1009 ACCCTCTTTATT 1021

RESULT 12
US-08-875-811-46
; Sequence 46, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1086 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1083
; OTHER INFORMATION: /note= "MetSerOnCangFv"
US-08-875-811-46

Query Match 35.7%; Score 267; DB 5; Length 1086;
Best Local Similarity 63.4%; Pred. No. 1.2e-75;
Matches 427; Conservative 0; Mismatches 240; Indels 6; Gaps 1;

QY 7 GATATCCAGATGACCCAGTCCCGCTCCCTGTCGCGCTCTGTGGCGGATAGGGTCACC 66
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QY 67 ATCACTGCGGCGCAGCGAAACATCTATGGCGCCCTGAATCGGTATCAACGTAAACCT 126
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Db 421 TTCACCTGCAAGCGAGTCAGGACATTAATACTATTATGCTGGTTCACGACAGAACCA 480
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QY 127 GGAAGAGCTCCGAGCTCTGATTACGGTGGCGACCACTGGCAGATGGAGTCCCTTCT 186
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```

NAME: Faris, Susan K.
 REGISTRATION NUMBER: 41,739
 REFERENCE/DOCKET NUMBER: 015280-244100US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 42:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1137 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..1137
 OTHER INFORMATION: /note= "SigpeplnncfBe6"
 US-08-875-811-42

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 487 TTCCTTGCAAGGCGGAGGAGGAGGAAACATCTATGCGCGCTGAACTGGTATCAACGTAA 546
 127 GGGAAAGCTCCGAGGCTTCTGATTTAGCGTGGAGCAACCTGGGCGGATAGGCTACC 186
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RESULT 14
 US-08-230-843-3
 Sequence 3, Application US/08230843
 Patent No. 5582826
 GENERAL INFORMATION:
 APPLICANT: SHIMAMURA, TOSHIO
 APPLICANT: HAMURO, JUNJI
 APPLICANT: NAKAZAWA, HARUMI
 APPLICANT: KANAYAMA, YUKA
 APPLICANT: SUGAMURA, KAZUO
 APPLICANT: TAKESHITA, TOSHIKAZU
 TITLE OF INVENTION: IMONOSUPPRESSANT
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: P. C.
 STREET: 1755 S. Jefferson Davis Highway, Suite 400
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/230,843
 FILING DATE: 21-APR-1994
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 094491/1993
 FILING DATE: 21-APR-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 036065/1994
 FILING DATE: 07-MAR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Oblon, No. 5582826man F.
 REGISTRATION NUMBER: 24,618
 REFERENCE/DOCKET NUMBER: 0010-0674-0X
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 413-3000
 TELEFAX: (703) 413-2220
 TELEX: 248855 OPAT UR
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 729 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: Other nucleic acid
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..729
 US-08-230-843-3

Query Match 33.5%; Score 250; DB 1; Length 729;
 Best Local Similarity 60.9%; Pred. No. 2.5e-70;
 Matches 447; Conservative 0; Mismatches 275; Indels 12; Gaps 2;

7 GATATCCAGATGACCCAGTCCCGTCTCCCTGTCGCGCTCTGTGGCGGATAGGCTACC 66
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QY 187 CGTTCTCTGGATCCGGCTCCGGAACGGATTCTACTCTGACCATCAGCAGCTGTCAGCCT 246
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QY 247 GAAGACTTCGCTAGCTATTACTGCTCAGAACGCTTTAAATATCTCCGTTGACCTTCGGACAG 306
Db 244 GAAGATTTGGGAGCTATTACTGCTCAACATTTTGGAGTACTCCGTCGACGCTTCGGTGA 303
QY 307 GGTACCAAGGTGGAATAAAGCTACTGGCGGTGGTGTCTTGGTGGGGGTGATCTGGT 366
Db 304 GGGACCAAGCTGGAGCTCAAA-----GTCGAGAAATCTCAGGATCTGGCTCCGAA 354
QY 367 GGTGGCGGTTCTCAAGTCCAACTGGTGAATCCGGCGCGGAGGTCAAGAACCCAGGGGCC 426
Db 355 TCCAAAAGCAGCAGCTCAAACTCGAGGAGTCTGGACCTGAGCTGGTGAAGCCTGGGGCT 414
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RESULT 15

US-08-636-936-3
; Sequence 3, Application US/08636936
; Patent No. 5856140
; GENERAL INFORMATION:
; APPLICANT: SHIMAMURA, TOSHIRO
; APPLICANT: HAMURO, JUNJI
; APPLICANT: NAKAZAWA, HARUMI
; APPLICANT: KANAYAMA, YUKA
; APPLICANT: SUGAMURA, KAZUO
; APPLICANT: TAKESHITA, TOSHIKAZU
; TITLE OF INVENTION: IMMUNOSUPPRESSANT
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; City: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/636,936
; FILING DATE: 24-APR-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/230,843

; FILING DATE: 21-APR-1994
; APPLICATION NUMBER: JP 094491/1993
; FILING DATE: 21-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 036065/1994
; FILING DATE: 07-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Obolon, No. 5856140man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 0010-0674-0X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 729 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..729
; US-08-636-936-3

Query Match 33.5%; Score 250; DB 3; Length 729;

Best Local Similarity 60.9%; Pred. No. 2.5e-70;

Matches 447; Conservative 0; Mismatches 275; Indels 12; Gaps 2;

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Db 355 TCCAAAAGCAGCAGCTCAAACTCGAGGAGTCTGGACCTGAGCTGGTGAAGCCTGGGGCT 414
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job time: 4667 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 12, 2000, 20:36:42 ; Search time 1890.83 Seconds

(without alignments)
707.902 Million cell updates/sec

Title: US-08-487-283a-12

Perfect score: 750

Sequence: 1 ATGAAGTGGAGCTGGGTAT.....GTGACAAACTGCACACATTA 750

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 972840 segs, 892348106 residues 1945680

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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5	476	63.5	18986	5 AR051652	AR051652 Sequence
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7	467.4	62.3	3282	5 AR038320	AR038320 Sequence
8	467.4	62.3	3282	5 I58595	I58595 Sequence 15
9	467.4	62.3	3282	5 I58609	I58609 Sequence 16
10	467.4	62.3	13254	5 AR038307	AR038307 Sequence
11	467.4	62.3	13254	5 AR038321	AR038321 Sequence
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13	467.4	62.3	13254	5 I58610	I58610 Sequence 17
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17	459.6	61.3	762	5 I87063	I87063 Sequence 57
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ALIGNMENTS

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cds.
ACCESSION M87789
VERSION M87789.1 GI:185361
KEYWORDS complementarity-determining region; constant region; immunoglobulin
gamma-chain; immunoglobulin heavy chain; variable region.
SOURCE Homo sapiens cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1599)
AUTHORS Lewis,A.P., Lemon,S.M., Barber,K.A., Murphy,P., Parry,N.R.,
Peakman,T.C., Sims,M.J., Worden,J. and Crowe,J.S.
TITLE Rescue, expression, and analysis of a neutralizing human
anti-hepatitis A virus monoclonal antibody
JOURNAL J. Immunol. 151 (5), 2829-2838 (1993)
MEDLINE 93367243
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polyA_signal
BASE COUNT 357 a 526 c 441 g 275 t
ORIGIN
Query Match 63.8%; Score 478.2; DB 9; Length 1599;
Best Local Similarity 78.0%; Pred. No. 7.6e-103;
Matches 595; Conservative 0; Mismatches 153; Indels 15; Gaps 1;
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RESULT 2

AR000007

LOCUS AR000007 9209 bp DNA PAT 04-DEC-1998

DEFINITION Sequence 3 from patent US 5736137.

ACCESSION AR000007

VERSION AR000007.1 GI:3962538

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 9209)

AUTHORS Anderson,D.R., Hanna,N., Leonard,J.E., Newman,R.A., Refl,M.E. and Rastetter,W.H.

TITLE Therapeutic application of chimeric and radiolabeled antibodies to human B lymphocyte restricted differentiation antigen for treatment

JOURNAL Patent: US 5736137-A 3 07-Apr-1998;

FEATURES Location/Qualifiers

source 1..9209

BASE COUNT 2239 a 2397 c 2390 g 2183 t

ORIGIN

Query Match 63.5%; Score 476; DB 5; Length 9209;

Best Local Similarity 78.2%; Pred. No. 2.5e-102;

Matches 385; Conservative 0; Mismatches 160; Indels 3; Gaps 1;

QY 1 ATGAAGTGAAGCTGGGTATCTCTCTCTGTCAGTACTGCGGCGCTCAGTCCAA 60
DB 2401 ATGGGTGAGACCTCATCTCTCTCTCTGTCAGTACTGCGGCGCTCAGTCCAA 2460
QY 61 GTCCACTGTGCAATCCGCGCGAGGTCAAGAACCCAGGCGCTCAGTCCAA 120
DB 2461 GTACAACTGCAAGACCTGGGCGTGAAGCTGGGCGCTCAGTCCAA 2520
QY 121 TGTAAAGTACGCGGTATATTTTCTATATGATTCATGGGTGCGTACGCCCC 180
DB 2521 TGTAAAGTACGCGGTATATTTTCTATATGATTCATGGGTGCGTACGCCCC 2580
QY 181 GGGCAGGCGCTGGAATGGATGGTGAATCTTACCGGCGCTGGAATGGATGGAT 240
DB 2581 GGTGCGGCGCTGGAATGGATGGTGAATCTTACCGGCGCTGGAATGGATGGAT 2640
QY 241 GAAATTTTAAAGACCGGTATATTTTCTATATGATTCATGGGTGCGTACGCCCC 300
DB 2641 GAAATTTTAAAGACCGGTATATTTTCTATATGATTCATGGGTGCGTACGCCCC 2700
QY 301 GAGCTTCACAGCTGCGATGGAGACAGCGCGCTGATATTTGCGCGCTTATTTT 360
DB 2701 GAGCTTCACAGCTGCGATGGAGACAGCGCGCTGATATTTGCGCGCTTATTTT 360
QY 361 GGTTCACCGCGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 420
DB 2759 -ACTACGCGGTGATCTTAAATGTTGGGCGCGAGGACGATGATGATGATGAT 2817
QY 421 AGCGCTTCACAGCGCGATGATTTTCTCTCTGCGCGCTGCTCTCAAGAGCACTCT 480
DB 2818 AGCGCTTCACAGCGCGATGATTTTCTCTCTGCGCGCTGCTCTCAAGAGCACTCT 2877
QY 481 GGGGCGACAGCGCGCTGCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 2878 GGGGCGACAGCGCGCTGCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2937

QY 541 TGTGGAAGTCAAGGCGCGCTGACAGCGCGGTGACACACTTCCGGGCTCTCTACAGTCC 600
DB 2938 TGTGGAAGTCAAGGCGCGCTGACAGCGCGGTGACACACTTCCGGGCTCTCTACAGTCC 2997
QY 601 TGAGAGCTTACTCCCTCAGCAGCGGTGAGCGGTGAGCGGTGAGCGGTGAGCGGTGAG 660
DB 2998 TGAGAGCTTACTCCCTCAGCAGCGGTGAGCGGTGAGCGGTGAGCGGTGAGCGGTGAG 3057
QY 661 ACTACATCTGCAAGCGTGAATCAAGAACCCAGACACCAAGGTGAGCAAGAAAGTTGAG 720
DB 3058 ACTACATCTGCAAGCGTGAATCAAGAACCCAGACACCAAGGTGAGCAAGAAAGTTGAG 3117
QY 721 CCCAAATCTTGACAAACTCACAAT 748
DB 3118 CCCAAATCTTGACAAACTCACAAT 3145

RESULT 3

AR015961

LOCUS AR015961 9209 bp DNA PAT 05-DEC-1998

DEFINITION Sequence 2 from patent US 5776456.

ACCESSION AR015961

VERSION AR015961.1 GI:3972238

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 9209)

AUTHORS Anderson,D.R., Hanna,N., Leonard,J.E., Newman,R.A., Refl,M.E. and Rastetter,W.H.

TITLE Therapeutic application of chimeric and radiolabeled antibodies to human B lymphocyte restricted differentiation antigen for treatment

JOURNAL Patent: US 5776456-A 2 07-Jul-1998;

FEATURES Location/Qualifiers

source 1..9209

BASE COUNT 2238 a 2395 c 2394 g 2182 t

ORIGIN

Query Match 63.5%; Score 476; DB 5; Length 9209;

Best Local Similarity 78.2%; Pred. No. 2.5e-102;

Matches 585; Conservative 0; Mismatches 160; Indels 3; Gaps 1;

QY 1 ATGAAGTGAAGCTGGGTATCTCTCTCTGTCAGTACTGCGGCGCTCAGTCCAA 60
DB 2401 ATGGGTGAGACCTCATCTCTCTCTCTGTCAGTACTGCGGCGCTCAGTCCAA 2460
QY 61 GTCCACTGTGCAATCCGCGCGAGGTCAAGAACCCAGGCGCTCAGTCCAA 120
DB 2461 GTACAACTGCAAGACCTGGGCGTGAAGCTGGGCGCTCAGTCCAA 2520
QY 121 TGTAAAGTACGCGGTATATTTTCTATATGATTCATGGGTGCGTACGCCCC 180
DB 2521 TGTAAAGTACGCGGTATATTTTCTATATGATTCATGGGTGCGTACGCCCC 2580
QY 181 GGGCAGGCGCTGGAATGGATGGTGAATCTTACCGGCGCTGGAATGGATGGAT 240
DB 2581 GGTGCGGCGCTGGAATGGATGGTGAATCTTACCGGCGCTGGAATGGATGGAT 2640
QY 241 GAAATTTTAAAGACCGGTATATTTTCTATATGATTCATGGGTGCGTACGCCCC 300
DB 2641 GAAATTTTAAAGACCGGTATATTTTCTATATGATTCATGGGTGCGTACGCCCC 2700
QY 301 GAGCTTCACAGCTGCGATGGAGACAGCGCGCTGATATTTGCGCGCTTATTTT 360
DB 2701 GAGCTTCACAGCTGCGATGGAGACAGCGCGCTGATATTTGCGCGCTTATTTT 360
QY 361 GGTTCACCGCGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 420
DB 2759 -ACTACGCGGTGATCTTAAATGTTGGGCGCGAGGACGATGATGATGATGATGAT 2817

0Y	1	ATGAAGTGGACCTGGGTTATTCCTTCTCCTCCGTGACAGTAATGGCGGCGTCCATCTCCAA	60
0Y	1		
Db	15	ATGAAATGACACTGGGTCTTCTCTTCTCTCTCTGACGTAATACAGGATGTCACATCCGAG	74
0Y	61	GTTCAACGTGTGCATATCCGGCGCCGAGGTCAAGCAAGCAGGGGCGCTACGTCAAGTGTCC	120
0Y	61		
Db	75	GTTACGCTGGTTCAGTCCGGGGCTGAGGTGAAGAACCTGGGGGCTCAGTGAAGAGTTTCT	134
0Y	75		

Query Match	62.3%	Score 467.4	DB 5	Length 3282
Best Local Similarity	78.7%	Pred. N. 2.7e-100		
Matches 577	Conservative	0	Mismatches 141	Indels 15
				Gaps 1

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source	1. .3282	/organism="unknown"
BASE COUNT	599 a	864 c 1109 g 710 t
ORIGIN		
Query Match	62.3%	Score 467.4; DB 5; Length 3282;
Best Local Similarity	78.7%	Pred. No. 2.7e-100;
Matches 577; Conservative	0; Mismatches 141; Indels 15; Gaps	
OY	1	ATGAATGAGCTGGGTTATTCCTCTTCCCTCGTAGTAACAGCCGGGCGTCCCA 60
Db	3268	ATGGAATGAGCTGGGTTCTTCTCTTCTTCTTCTCGTAGTAACAGAGTCTCCAG 3209
OY	61	GTCACAGTGTGTCATTCGGCGCCGAGGTCAAGAACGAGGGGCTCAGTCAAGTGC 120
Db	3208	GTTCAAGTGTGTCATTCGGGCGCTGAGGTGAAGAACGCTGGGGCTCAGTGAAGTTCT 3149
OY	121	TGTAAAGCTAGGCGGTATATTTTCTAATTGTGGATTCATGGGTGGTCAAGCCCC 180
Db	3148	TGTCAAGCTCTGATACAGATTCAGTACATTTGTTATTCATTTGGGTGGCGCCGCC 3089
OY	181	GGGCGAGGCTGGAATGATGGGTGAGATCTTACCGGGCTGTGTAGACACCAATATAC 240
Db	3088	GGACGAGGTTGATGTGATGGGATGAGATCACTCTTACACGGAAGAAATTTTCA 3029
OY	241	GAATAATTTAAAGACCGTGTATCTATGACGCGTGACACTTGCAGTACAGTATACATG 300
Db	3028	GCGAAGTTCAGAGACAGATCACCTTTACCGCGGACACATCCGCAACACAGCTACATG 2969
OY	301	GAGCTCTCAGCGCTGCGATCCGAGACACGCGGCTATATTTGGCG----- 348
Db	2968	GAGTTGAGAGGCTCAGGCTGACAGACACGCGCTGTTATTTATTTGTCAGAGTGGGCCA 2909
OY	349	--CGTATTTTGTGTTCTAGCCCAATGTGATTTGATGTTGGGCTCAAGAAC 405
Db	2908	TATATTTGGGATGATTTCTCCAGACAAATTTATATATGACGTCTGGGCAAGAAC 2849
OY	406	CTGTCTACTGTCTGAGCGCTCCACCAAGGGCCCATGGTCTTCCCTCGCGGCTCC 465
Db	2848	ACGGTCATCTGTAGCTCAGCTCCACCAAGGGCCCATGGTCTTCCCTCGCACCTCC 2789
OY	466	TCCAGACACCTCTGCGGGGCGACACCGGCTCTGGGCTGCTGTGTAAAGATCTATTCCC 525
Db	2788	TCCAGACACCTCTGCGGGGCGACACCGGCTCTGGGCTGCTGTAAAGATCTATTCCC 2729
OY	526	GAACCGGTGACGGTCTGCGAAGTCAAGGCGCTTGACACGCGGCTGACACCTTCCG 585
Db	2728	GAACCGGTGACGGTCTGCGAAGTCAAGGCGCTTGACACGCGGCTGACACCTTCCG 2669
OY	586	GCTGTCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCCTCAGC 645
Db	2668	GCTGTCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCCTCAGC 2609
OY	646	AGCTTGGGCAACCACTACATCTGCAACGTGAATCACAAAGCCACGCAACCAAGGTG 705
Db	2608	AGCTTGGGCAACCACTACATCTGCAACGTGAATCACAAAGCCACGCAACCAAGGTG 2549
OY	706	GACAGAAGTGTG 718
Db	2548	GACAGAAGTGTG 2536
RESULT 10		
LOCUS	AR038307	
DEFINITION	Sequence 156 from patent US 5804440.	
ACCESSION	AR038307	
VERSION	AR038307.1	GI:5957024
KEYWORDS	Unknown.	
SOURCE	Unknown.	
ORGANISM	Unknown.	
	Unclassified.	

REFERENCE	1 (bases 1 to 13254)
AUTHORS	Burton,D.R., Barbas,C.F. and Lerner,R.A.
TITLE	Human neutralizing monoclonal antibodies to human immunodeficiency virus
JOURNAL	Patent: US 5804440-A 156 08-SEP-1998;
FEATURES	Location/Qualifiers
SOURCE	1..13254
BASE COUNT	/organism="unknown" 3206 a 3559 c 3251 g 3238 t
ORIGIN	

[illegible]

Query Match	62.3%	Score 467.4	DB 5	Length 13254
Best Local Similarity	78.7%	Pred. No. 2.7e+100		
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Qy 1	ATGAAGTGGAGCTCGGTTATTCTCTCTCTGTCAAGTAACGCGGGCTGCACCTCCAA 60			
Db 2450	ATGAAGTGGAGCTGGGTCTTCTCTCTCTGTCAAGTAACGAGGTGCCACTCCGAG 2509			
Qy 61	GTTCAAAGTGGTGCAAATCCGGCGCGAGGTCAAGAAGCCAGCGGGCTCAGTCAAAAGTGTCC 120			
Db 2510	GTTCAAGTGGTTCAGTCCGGGGCTGAGTGAAGAAGCTGGGGCTCAGTGAAGGTTCCT 2569			
Qy 121	TGTAAGCTACGGCTATATATTTTCTAAATATTGGATTAATGGTGGCTGACGCCCCC 180			
Db 2570	TGTCAGGCTTCTGATACAGATTCAAGTAACCTTGTATTTCATTGGGTGCGCAGGCCCCC 2629			
Qy 181	GGGAGGSCCTGGAAATGGATGGTGGATCTTACCGGGCTCTGGTAGACACGAATATACC 240			
Db 2630	GGACAGAGTGTGGATGGATGGATGGATCAATCCTTACAACGGAAACAAGAATTTTCA 2689			
Qy 241	GAATTTTAAAGACCGTGTACTATACGGCTGACACTTCGACTAGTACAGTATACATG 300			
Db 2690	CGGAAGTCCAGGACAGATCAACCTTTACCGCGACACATCCGCGACACAGCCTACATG 2749			
Qy 301	GAGCTCTCCAGCCTCGCATCGGAGACACGCGCCTTATTATTGCGCG - - - - - 348			
Db 2750	GAGTTGAGGACCTCAGGCTCGACACACGCGCTGTATTATTATGTCGAGAGTGGGGCCA 2809			
Qy 349	--CGTATTTTTTGGTCTTAGCCGGAATGGTATTTTGATGTTGGGTCAAGGAACC 405			
Db 2810	TATAGTTGGGATGATCTCCCGACCAATATTATATATGAGCGCTGTGGGCAAGGAACC 2869			
Qy 406	CTGCTCACTGCTCGAGGCGCTCCACCAAGGGCCCATCGGCTTCTCCCTCTGGCGCCCTCC 465			
Db 2870	ACGCTATCGTGAGCTCAGCTTCCACCAAGGGCCCATCGGCTTCTCCCTCTGGCACCTCC 2929			
Qy 466	TCCAAGAGCACTCTGGGGGACACGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC 525			
Db 2930	TCCAAGAGCACTCTGGGGGACACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC 2989			
Qy 526	GAACGGTGACGGTGTGTTGGAATCAGGCGCCCTGACACGGGGGTGCACACCTTCCCG 585			
Db 2990	GAACGGGTGACGGTGTCTGTGAATTCAGGCGCCCTGAGCAGCGGGCTGCACACCTTCCCG 3049			
Qy 586	GCTGCTCTACAGTCTCTCAGGACTCTACTTCCCTCAGCAGCGTGGTACCGTGCCTCCAGC 645			
Db 3050	GCTGCTCTACAGTCTCTCAGGACTCTACTTCCCTCAGCAGCGTGGTACCGTGCCTCCAGC 3109			
Qy 646	AGCTGGGCAACCCAGACCTACATCTGCAACGTGAATCAACAGCCCGACCAACCAAGGTG 705			

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Db 3110 AGCTTGGGACCCACAGCTACATCTGCAACGTGAATCACAAGCCCAAGCAACCAAGGTG 3169
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Qy 706 GACAGAAGTTG 718
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Db 3170 GACAGAAGTTG 3182

RESULT 13
LOCUS 158610 13254 bp DNA PAT 07-OCT-1997
DEFINITION Sequence 170 from patent US 5652138.
ACCESSION 158610
VERSION 158610.1 GI:2477848
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 13254)
AUTHORS Burton,D.R., Barbas,C.F. and Lerner,R.A.
TITLE Human neutralizing monoclonal antibodies to human immunodeficiency
        virus
JOURNAL Patent: US 5652138-A 170 29-JUL-1997;
FEATURES
        Location/Qualifiers
SOURCE 1..13254
BASE COUNT 3238 a 3251 c 3559 g 3206 t
ORIGIN

Query Match 62.3%; Score 467.4; DB 5; Length 13254;
Best Local Similarity 78.7%; Pred. No. 2.7e-100;
Matches 577; Conservative 0; Mismatches 141; Indels 15; Gaps 1;

Qy 1 ATGAAGTGGAGCTGGGTTATCTCTCTCTCTGTCAGTACTGCCGGCTGCACCTCCAA 60
      |||||||
Db 10805 ATGAATGAGCTGGGCTTCTCTCTCTCTCTGTCAGTACTGAGTACTGCCAGC 10746
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Qy 61 GTCCAACTGTCGCAATCCGGGGCCAGGTCAAGAACCCAGGGGCTCATCAAGTGTCC 120
      |||||||
Db 10745 GTTACGCTGTTCACTCCGGGGCTGAGTGAAGAACCTCGGGGCTCATGAGGTTCT 10686
      |||||||

Qy 121 TGTAAAGCTACGCTATATTTTCTATATTTGATTCATGGGTGCGTCAAGGCCCC 180
      |||||||
Db 10685 TGTCAAGCTTCTGATACAGATTCAGTACTTGTATTCATGGGTGCGGCAAGGCCCC 10626
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Qy 181 GGGCAGGGCTGGAATGGATGGGTAGATCTTACCGGGCTGTGTAGCAACCAATATAC 240
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Db 10625 GGACAGAGTTGAGTGGATGGATGATCAATCTTACAAAGCAAAATTTTCA 10566
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Qy 241 GAAATTTTAAAGACCGTGTACTATGACGCTGACACTTCGACTAGTACATATCATG 300
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Db 10565 GCGAAGTCCAGGACAGAGTACCTTTACCGGGACACATCCGCGAACACAGCTTACATG 10506
      |||||||

Qy 301 GAGCTCTCAGCTGCGATCGGAGGACAGGGGCTGTATTTATTTGGCG- 348
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Db 10505 GAGTTGAGAGCTCAGCTCTGACAGACAGGCTGTTTATTTATTTGCGAGATGGGCCA 10446
      |||||||

Qy 349 --CGTATTTTGTGTTCTAGCCCAATTTGATTTTGTGTTGGGTCAAGGAC 405
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Db 10445 TATAGTTGGATGATTCCTCCAGAGCAATTTATATGAGAGTCTGGGGCAAGGAAC 10386
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Qy 406 CTGTCTACTGCTGACGGCTCCACCAAGGGCCATGGGTCTTCCCTGGGCGCTCC 465
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Db 10385 ACGGTCACTGTGAGCTCGCTTCCACCAAGGGCCATCGCTTCCCTGGGCGCTCC 10326
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Qy 466 TCCAGAGACACTCTGGGGGGACAGGGGCTGGGGCTGCTGCTGAAGACACTATCCCC 525
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Db 10325 TCCAGAGACACTCTGGGGGGACAGGGGCTGGGGCTGCTGCTGAAGACACTATCCCC 10266
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Qy 526 GAACCGGTGACGTGTCTGGAATCAGAGGCCCTGACAGGGGGGTGACACCTTCCG 585
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Db 10265 GAACCGGTGACGTGTCTGGAATCAGAGGCCCTGACAGGGGGGTGACACCTTCCG 10206
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Qy 586 GCTGTCTTACAGTCTCTAGAGACTCTACTCCCTCAGAGCGTGGTGAACCTGCCACAGC 645
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Qy 646 AGCTTGGCACCCACCAAGCTTACATCTGCAACGTGAATTCACAGCCCAACCAAGGTG 705
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Qy 706 GACAGAAGTTG 718
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Db 10085 GACAGAAGTTG 10073

RESULT 14
LOCUS 169485 762 bp DNA PAT 04-FEB-1998
DEFINITION Sequence 57 from patent US 5677426.
ACCESSION 169485
VERSION 169485.1 GI:2831607
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 762)
AUTHORS Fong,S., Hebert,C.Alice, Kim,K.Jin and Leong,S.R.
TITLE Anti-IL-8 antibody fragments
JOURNAL Patent: US 5677426-A 57 14-OCT-1997;
FEATURES
        Location/Qualifiers
SOURCE 1..762
BASE COUNT 183 a 224 c 186 g 169 t
ORIGIN

Query Match 61.3%; Score 459.6; DB 5; Length 762;
Best Local Similarity 76.8%; Pred. No. 1.9e-98;
Matches 561; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

Qy 21 TCTCTTCTCTCTGTCAGTAACTCCGGGCTGCACCTCCCAAGTCCAACTGTCGAATCCG 80
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Qy 81 CCGCGAGTCAAGAACCCAGGGGCTCTACATCAAGTGTCTGTAAAGCTAGCGGCTATAT 140
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Db 93 ACCTGAGCTGATGAACCTGGGGCTTCAAGTGAAGATATCTGGAAGGCTTCTGTATATTC 152
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Qy 141 TTTTCTAATTTATTTGATTCATGAGGTGCTCAGAGCCCGGGCAGGGGCTGGAATGAT 200
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Db 153 ATTCAGTAGCCACTACATGACACTGGGTGAAGACAGACCATGAAAGCCTTGAGTGGAT 212
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Qy 201 GGGTGAATCTTACCGGGCTGTGTAGCACCAGATATACGAAATTTTAAAGACCGTGT 260
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Db 213 TGCGTCAATGATTCCTTCCAAATGTGAATGTAATCTTACCAAGAAATTTCAAGGGCAAGC 272
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Qy 261 TACTATAGACCGGTGAACACTTCACTAGTACATGATGATGAGACTCTCCAGCTGTGAT 320
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Db 273 CACATTTGACTGTGACACATCTTCCAGACAGCAACGTGCATCTCAGCAGCTGTGATC 332
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Qy 321 GGAGGACAGGGGCTGTATTTATTTGCGGCTGTATTTTGTGTTCTGAGCCGAATGGTA 380
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Db 333 TGTATGACTGTGCACTATTTCTGTGTGCAAGAGGGGACTATAGATACACGGGCAATGGT 392
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Qy 381 TTTTGAATTTTGGGTCAAGGAACCTGTGTACTGTCTGAGGCGCTCCACCAAGGGCC 440
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Db 393 TTTGATGATCTGGGGGGCAGAGGACACAGGTACACGTCCTCTCCGCTCCACCAAGGGCC 452
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Qy 441 ATGGGTCTTCCCTGGGCGCTCTCTCAAGAGACACTCTGGGGGACAGGGGCTTGGG 500
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Db 453 ATGGGTCTTCCCTGGGCGCTCTCTCAAGAGACACTCTGGGGGACAGGGGCTTGGG 512
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Qy 501 CTGCTGTGCAAGACTACTTCCCGAAGCGGTGAAGGTTCTGAGAACTCAGGGCGCT 560
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Db 513 CTGCTGTCTAAGGACTACTTCCCGGAACCGGTGACGGTGTCTGGAACCTCAGGCGCCCT 572
QY 561 GACCAGCGGTGCACACCTTCCCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAG 620
Db 573 GACCAGCGGTGCACACCTTCCCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAG 632
QY 621 CAGCGTGTGACCGTGTCCAGAGCTTGGGCAACCCAGAGCTTACATCTGCAAGGTGAA 680
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QY 681 TCACAAGCCCGAGCAACAGGTGGCAAGAAAGTTGAGCCCAATCTTGTGACAAAAC 740
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QY 741 TCACACATAA 750
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LOCUS I73104 762 bp DNA PAT 03-APR-1998
DEFINITION Sequence 57 from patent US 5686070.
ACCESSION I73104
VERSION I73104.1 GI:3009243
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 762)
AUTHORS Doerschuk,C.M., Fong,S., Hebert,C.Alice, Kim,K.Jin and Leong,S.R.
TITLE Methods for treating bacterial pneumonia
JOURNAL Patent: US 5686070-A 57 11-NOV-1997;
FEATURES
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1. 762
/organism="unknown"
BASE COUNT 183 a 224 c 186 g 169 t
ORIGIN

Query Match 61.3%; Score 459.6; DB 5; Length 762;
Best Local Similarity 76.8%; Pred. No. 1.9e-98;
Matches 561; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY 21 TCTCTCTCTCTGTCAGTAACCTGCGGGTCCACCTCCCAAGTCCAACTCGTGGCAATCCGG 80
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Db 93 ACCTGAGCTGATGAAGCCTTGGGGCTTCACTGAAGATATCTTCAAGGCTTCTGGTTATTTC 152
QY 141 TTTTCTAATTATTGGATTCAATGGTGTGCGTCCAGGCCCCCGGCGGCGCTGGAATGGAT 200
Db 153 ATTCAAGTACCACTACATGCACTGGTGAAGCAGAGCCATGGAAAGAGCCTTGAGTGGAT 212
QY 201 GGGTGAGATCTTACCGGGCTCTGGTAGCAGCCGAATATACCGAAAATTTAAAGACCGTGT 260
Db 213 TGGTACATTTGATCTTCCAATGGTGAAGTACTTACACACCAAGAAATTCAGGGCAAGGC 272
QY 261 TACTATGACGCTGACACTTCGACTAGTACATATACATGAGAGCTCTCCAGGCTGCGATC 320
Db 273 CACATTGACTGAGACACATCTCCAGCACACCCAAAGTGCATCTCAGCAGGCTGACATC 332
QY 321 GGAGSACACGGCGCTATTATTATGGCGCGTTATTTTTTGGTTCTAGCCCGAATTTGGTA 380
Db 333 TGATGACTCTGCAGTCTATTTCTGTGCAAGAGGGGACTATAGATACAACGGGCGACTGGTT 392
QY 381 TTTTGATGTTGGGGTCAAGGAACCGCTGGTCACTGTCTCGAGCGCTCCACCAAGGGCCC 440
Db 393 TTTTCGATGCTGGGGCGCAGGAGCACCGGTCAACCGTCTCTCCGCGCTCCACCAAGGGCCC 452
QY 441 ATCGGTCTTCCCGCTGGGCGCCCTCTCCAAAGAGCAGCTCTGGGGGCGACAGCGGCCCTGGG 500

Db 453 ATCGGTCTTCCCGCTGGCACCCCTCTCCCAAGAGCACCTCTGGGGGCGACAGCGCCCTGGG 512
QY 501 CTGCGCTGGTCAAGGACTACTTCCCGGAACCGGTGACGGTGTCTGGAACCTCAGGCGCCCT 560
Db 513 CTGCGCTGGTCAAGGACTACTTCCCGGAACCGGTGACGGTGTCTGGAACCTCAGGCGCCCT 572
QY 561 GACCAGCGGTGCACACCTTCCCGGCTGTCTCTACAGTCTCAGGACTCTACTCCCTCAG 620
Db 573 GACCAGCGGTGCACACCTTCCCGGCTGTCTCTACAGTCTCAGGACTCTACTCCCTCAG 632
QY 621 CAGCGTGTGACCGTGTCCCGTCCAGCAGCTTGGGCAACCCAGAGCTTACATCTGCAAGGTGAA 680
Db 633 CAGCGTGTGACCGTGTCCCGTCCAGCAGCTTGGGCAACCCAGAGCTTACATCTGCAAGGTGAA 692
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QY 741 TCACACATAA 750
Db 753 TCACACATGA 762

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Job time: 4665 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 12, 2000, 20:04:48 ; Search time 930.19 Seconds
(without alignments)
3555.587 Million cell updates/sec

Title: us-08-487-283a-12
Perfect score: 750
Sequence: 1 ATGCAAGTGGAGCTGGGTTAT.....GTGACAAACTCACAATAA 750

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5247842 seqs, 2204914090 residues

Total number of hits satisfying chosen parameters: 10495684

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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41: gb_est22:*
42: gb_est23:*
43: gb_est24:*

44: gb_est25:*
45: gb_est26:*
46: gb_est27:*
47: gb_est28:*
48: gb_est29:*
49: em_est20:*
50: em_est21:*
51: em_est22:*
52: gb_est30:*
53: gb_est31:*
54: gb_est32:*
55: em_est23:*
56: em_est24:*
57: em_est25:*
58: em_est26:*
59: gb_est33:*
60: gb_est34:*
61: gb_est35:*
62: gb_est36:*
63: gb_est37:*
64: gb_est38:*
65: em_est27:*
66: em_est28:*
67: em_est29:*
68: em_est30:*
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80: gb_est46:*
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96: gb_est59:*
97: em_est38:*
98: em_est39:*
99: em_est40:*
100: em_est41:*
101: gb_est60:*
102: gb_est61:*
103: em_est42:*
104: em_est43:*
105: gb_est62:*
106: gb_est63:*
107: gb_est64:*
108: em_est44:*
109: em_est45:*
110: gb_est65:*
111: gb_est66:*
112: em_est46:*
113: em_est47:*
114: em_est48:*
115: em_est49:*
116: gb_est67:*

Db 356 CTCCTCAGACAGCGTGTGACCTGCCCTTCACAGACTGTGGGACCCAGACCTACATCTG 415

Qy 672 CAACGTGAATCAACAGCCAGCAACAGTGTGACAGAAAGTTGAGCCCAATCTTG 731

Db 416 CAACGTGAATCAACAGCCAGCAACAGTGTGACAGAAAGTTGAGCCCAATCTTG 475

Qy 732 TGACAAACTCACA 745

Db 476 TGACAAACTCACA 489

RESULT 2

AM606355 669 bp mRNA EST 23-MAR-2000

LOCUS QV0-HTC366-280100-088-b12 HT0366 Homo sapiens cDNA, mRNA sequence.

DEFINITION AM606355

ACCESSION AM606355.1 GI:7311096

KEYWORDS EST.

ORGANISM human.

SOURCE Homo sapiens

REFERENCE 1 (bases 1 to 669)

AUTHORS HCEP <http://www.ludwig.org.br/ORESTES>.

TITLE The FAPESP/LICR Human Cancer Genome Project

JOURNAL Unpublished (1999)

COMMENT On May 7, 1998 this sequence version replaced g1:3118821.

Contact: Simpson A.U.G.

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Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV0&t2=QV0-HT0366-280100-088-b12&t3=2000-01-28&t4=1>)

Seq primer: puc 18 forward

High quality sequence start: 10

High quality sequence stop: 661.

Location/Qualifiers

1. 669

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="HT0366"

/dev_stage="Adult"

/note="Organ: head_neck; Vector: puc18; Site:1: SmaI; Site:2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 160 a 191 c 185 g 133 t

ORIGIN

Query Match 47.8%; Score 358.4; DB 74; Length 669;

Best Local Similarity 73.8%; Pred. No. 3.7e-91;

Matches 493; Conservative 0; Mismatches 151; Indels 24; Gaps 2;

Qy 100 GGGGCGCTCAGTCAAGTGTCTGTAAAGCTAGCGGCTAATTTTCTAATTAATTTGATT 159

Db 1 GGGGCGCTCCCGAGATCTCTGTGCACTCTGATTTATTTTGTAAATACTAGACT 60

Qy 160 CAATGGTCTCAGAGCCCGGCGGAGGCGCTGGAATGATGGTGAATCTTACCGGGC 219

Db 61 GACCTGTGGTTCGCGAGCTCCAGGAGGCGCTGAGGCGGCAATATAGACGAAGAT 120

Qy 220 TCTGTAGCAGCAATATACCGAAATTTTAAAGACGCTGTACTATGAGCGGTGACACT 279

Db 121 GGAAGTGAACAACTATGTGGACTGTGTGAAGGGCCGATTCCACATCTCCAGGACAC 180

Qy 280 TCGAGTACTACATATACATGAGCTCTCCAGCTGCGATGAGAGACGGCCGTAT 339

Db 181 GCCGAGAGTACCTATCTACTGCAATATGACAGCTGAGAGGGGAGACAGCGGTATAT 240

Qy 340 TATTGGCGCG-----TTATTTTGGTGTCTAGCCGAAATG 377

Db 241 TACTGTGCGAGAGAAAAAAGGTCGATTACGACTTTTGAATGGTATCAAAACAAATGA 300

Qy 378 GTATTTGATGTGGGTCAAGAACCTGTCTACTCTCTGAGCGCTCCACCAAGG 437

Db 301 TCGTTGATGTCTGGGGCCAGGACATGTCTCTCTTCCAGCTCCACCAAGG 360

Qy 438 CCCATCGCTTCCCGCTGGGCGCCCTCTCCAGAGACACTCTGGGGGACAGCGGCCCT 497

Db 361 CCCATCGCTTCCCGCTGGGCGCCCTCTCCAGAGACACTCTGGGGGACAGCGGCCCT 420

Qy 498 GGGCTGCTGTCAAGACTACTTCCCGAACCGGTGACGGTGTCTGGAATCAGGCGC 557

Db 421 GGGCTGCTGTCAAGACTACTTCCCGAACCGGTGACGGTGTCTGGAATCAGGCGC 480

Qy 558 CCGTACACAGCGCGGTGCAACACTTCCGGCTGTCTTACAGTCTCAGACTCTACTCCT 617

Db 481 CCTACACAGCGCGGTGCAACACTTCCGGCTGTCTTACAGTCTCAGACTCTACTCCT 540

Qy 618 CAGAGCGTGTGACCGGCTCCAGAGCTGTGGGACCCAGACTCTATCTGACACT 677

Db 541 CAGAGCGTGTGACCGGCTCCAGAGCTGTGGGACCCAGACTCTATCTGACACT 600

Qy 678 GAATCACAAGCCCAACACCAAGTGTGACAGAAAGTTGAGCCCAATCTTGTGACAA 737

Db 601 GAATCACAAGCCCAACACCAAGTGTGACAGAAAGTTGAGCCCAATCTTGTGACAA 658

Qy 738 AACTCACA 745

Db 659 AATCACA 666

RESULT 3

AM404758 564 bp mRNA EST 16-FEB-2000

LOCUS UI-HF-BLO-acd-h-05-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone

DEFINITION IMAGE:3058808 5', mRNA sequence.

ACCESSION AM404758

VERSION AM404758.1 GI:6923815

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 564)

AUTHORS NIH-MGC <http://www.ncbi.nlm.nih.gov/MGC/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M.B. Soares Lab

cDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: www-bio.liml.gov/bdrp/image/image.html

Seq primer: M13 forward

Location/Qualifiers

1. 564

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:3058808"

/clone_lib="NIH_MGC_37"

FEATURES

source

/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"

/note="Vector: pT7f3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

119 a 210 c 138 g 97 t

BASE COUNT
ORIGIN

Query Match 47.3%; Score 355; DB 72; Length 564;

Best Local Similarity 84.8%; Pred. No. 3.3e-90;

Matches 413; Conservative 0; Mismatches 65; Indels 9; Gaps 1;

QY 262 ACTATGACGGGTGACACTTCGACTAGTACAGTATACATGAGGCTCTCCAGCGCTCGCATCG 321

Db 2 ACGAGGTACGGCGCAGCAAGTCCATCAACACCGCTACCTGAGTGAGCAGCTGAAGGCC 61

QY 322 GAGGACAGCGGCTCTATATATGCGGCGGTATTTTGGTCTAGCCGAATGGTAT 381

Db 62 TCGGACACCGCCATTATTAATGCTGCGAGACCCCT-----CAGCGGTGGCTGGCCC 112

QY 382 TTGTATGTTGGGTCAAGGAACCTGGTCACTGCTCTGAGCGCTCCACCAAGGGCCCA 441

Db 113 CTGTAGTACTGGGGCCAGGAACCTGGTCACTGCTCTGAGCGCTCCACCAAGGGCCCA 172

QY 442 TGGGTCTTCCCGCTGGCGGCTCTCAAGAGCACCTCTGGGGCAGAGGGCCCTGGGC 501

Db 173 TCGGTCTTCCCGCTGGCGGCTCTCAAGAGCACCTCTGGGGCAGAGGGCCCTGGGC 232

QY 502 TGCCTGGTCAAGGACTACTTCCCGGAACCGGTGACGTGCTGGAACCTCAGGCGCCCTG 561

Db 233 TGCCTGGTCAAGGACTACTTCCCGGAACCGGTGACGTGCTGGAACCTCAGGCGCCCTG 292

QY 562 ACCAGGGGGTGACACCTTCCCGGCTGCTCAGAGTCTTCCAGGACTCTACTCCCTCAGC 621

Db 293 ACCAGGGGGTGACACCTTCCCGGCTGCTCAGAGTCTTCCAGGACTCTACTCCCTCAGC 352

QY 622 AGGTGGTGAACCTGCGCTCCAGGAGTGGGCAACCGAGCTACATCTGCAAGTGAAT 681

Db 353 AGGTGGTGAACCTGCGCTCCAGGAGTGGGCAACCGAGCTACATCTGCAAGTGAAT 412

QY 682 CACAAGCCAGCAACCAAGGTGGACAAGAAAGTTGAGCCCAATCTTGACAAAACT 741

Db 413 CACAAGCCAGCAACCAAGGTGGACAAGAAAGTTGAGCCCAATCTTGACAAAACT 472

QY 742 CACACAT 748

Db 473 CACACAT 479

RESULT 4

AW378707 581 bp mRNA EST 04-FEB-2000
LOCUS PM2-HT0225-031299-003-b01 HT0225 Homo sapiens cDNA, mRNA sequence.
DEFINITION
ACCESSION AW378707
VERSION AW378707.1 GI:6883366
KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 581)

AUTHORS HCGP <http://www.ludwig.org.br/ORESTES>.

TITLE The FAPESP/LICR Human Cancer Genome Project

JOURNAL Unpublished (1999)

COMMENT On Feb 10, 1999 this sequence version replaced gi:4061421.

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM2&t2=PM2-HT0225-031299-003-b01&t3=1999-12-03&t4=1>)

Seq primer: puc 18 forward

High quality sequence start: 13

High quality sequence stop: 575.

Location/Qualifiers

FEATURES

source

1. 581

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="HT0225"

/dev_stage="Adult"

/note="Organ: head_neck; Vector: puc18; Site_1: SmaI;

Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

113 a 189 c 160 g 119 t

BASE COUNT

ORIGIN

Query Match 47.0%; Score 352.8; DB 71; Length 581;

Best Local Similarity 80.3%; Pred. No. 1.4e-89;

Matches 427; Conservative 0; Mismatches 102; Indels 3; Gaps 1;

QY 163 TGGGTGCGCTCAGGCGCCCGGCGGCTGGAATGGATGGGTGAGATCTTACGGGCTCT 222

Db 45 TGGGTGCGGCGAGGCGCCCTGGCAAGGCTTGAGTGGGTGGGAAGATATTCCTTTGGCT 104

QY 223 GGTAGCACCAATATACCGAAATTTTAAAGACCTGTACTATGACCGGTGACACTTCG 282

Db 105 GGTATCGGATACTAGCGTAAGAAATTCCTGGACAGAATCACAAATTACCGGACATGTCT 164

QY 283 ACTAGTACAGATATACATGGAGCTCTCCAGCTCGGATCGGAGCACGCGCTCTATTAT 342

Db 165 GCGGCCACAGCCTCTTGGAGGTGAACACCTCCGATCTGAGGACACGCGCTCTACTAC 224

QY 343 TCGCGCGCTTATTTTGGTTCTAGCCCGAATGGTATTTTGTATGTTTGGGGTCAAGA 402

Db 225 TGTGTGCGACATAGAAGTGGTGACAATC---TTGCACCTTTTGTATGTTGGGGCTCGGA 281

QY 403 ACCCTGGTCACTGCTCGAGCGCCTCCACCAAGGCGCCATCGGCTTCCCTCGGCGCC 462

Db 282 ACTTCCGTCCGCTCTGCGAGCCTCCACCAAGGCGCCATCGGCTTCCCTCGGCGCC 341

QY 463 TCCTCCAAGAGCACCTCTGGGGGACAGCGGCTGGGCTGCTGGTCAAGGACTACTTC 522

Db 342 TCCTCCAAGAGCACCTCTGGGGGACAGCGGCTGGGCTGCTGGTCAAGGACTACTTC 401

QY 523 CCGCAACCGGTGACGCTGCTGGAACTCAGCGGCCCTGACACGCGGCTGACACCTTC 582

Db 402 CCCGAACCTGGTGACGCTGCTGGAACTCAGCGGCCCTGACACGCGGCTGACACCTTC 461

QY 583 CCGGCTGCTTACAGTCTCTCAGGACTCTACTCCCTCAGCAGGCTGGTGCCTGCCCTCC 542

Db 462 CCGGCTGCTTACAGTCTCTCAGGACTCTACTCCCTCAGCAGGCTGGTGCCTGCCCTCC 521

QY 643 AGCAGCTTGGGCGCCAGACCTACATCTGCAACGTGAATCAACAGCCAGCA 694

Db 522 AGCAGCTTGGGCGCCAGACCTACATCTGCAACGTGAATCAACAGCCAGCA 573

RESULT 5

AW381291

LOCUS

AW381291

683 bp

mRNA

EST

04-FEB-2000

DEFINITION	RC0-HT0298-201199-011-f08 HT0298 Homo sapiens cDNA, mRNA sequence.
ACCESSION	AM381291
VERSION	AM381291.1 GI:6885950
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 683)
TITLE	HCCP http://www.ludwig.org.br/ORSTES .
JOURNAL	The FAPESP/LICR Human Cancer Genome Project
COMMENT	Unpublished (1999) On May 18, 1998 this sequence version replaced gi:3136800. Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL. (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC0&t2=RC0-HT0298-201199-011-f08&t3=1999-11-20&t4=1) Seq primer: puc 18 forward High quality sequence start: 15 High quality sequence stop: 657. Location/Qualifiers
FEATURES	
source	<pre>1..683 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="HR0298" /dev_stage="Adult" /note="Organ: head,neck; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."</pre>
BASE COUNT	146 a 224 c 181 g 132 t
ORIGIN	
Query Match	47.0%; Score 352.2; DB 71; Length 683;
Best Local Similarity	86.6%; Pred. No. 2.2e-89;
Matches 401; Conservative	0; Mismatches 58; Indels 4; Gaps 1;
OY	290 CAGTTACATGAGAGCTCCACCCCTGCGATCGAGACACAGCGCCCTCATTA--TTGC 345
Db	6 CACTGTATCTCGAAATGGAACACGCTGAGAGCTGAGACACACGCTGTGTAATCTGTGCTC 65
OY	346 GCGCGTATATTTTGGTTCGAGCCCGAATGGATTTGATGTGGGGTCAAGAAC 405
Db	66 CCAGCCCTTATGATAGTAGTAGTGTATTTCTTACTACGTTTGACTGTGGGCCAGGAACC 125
OY	406 CTGGTCACTGTCTCGAGCGCCCTCCACCAAGGGCCCATGGTTCCTCCCGCGCCCTCC 465
Db	126 CTGGTCACTGTCTCGAGCGCCCTCCACCAAGGGCCCATGGTTCCTCCCGCGCCCTCC 185
OY	466 TCACAAGACACCTCTGGGGGGCACAGCGCCCTGGGCTGCTGTCAGAGACTTCTCCG 525
Db	186 TCACAAGACACCTCTGGGGGGCACAGCGCCCTGGGCTGCTGTCAGAGACTTCTCCG 245
OY	526 GAACCGGTGAGCGGTCTGTGGAACACAGGCGCCCTGACACAGGGGTGACACACTTCCG 585
Db	246 GAACCGGTGAGCGGTCTGTGGAACACAGGCGCCCTGACACAGGGGTGACACACTTCCG 305
OY	586 GGTGCTCTACAGTCTCTCAGAGACTTACATCCCTCAGACAGGTGATACCGGTGCCCTCAGC 645
Db	306 GGTGCTCTACAGTCTCTCAGAGACTTACATCCCTCAGACAGGTGATACCGGTGCCCTCAGC 365

QY	646	ACCTGGGGACCCAGACACCTACATCTGCGAACCCTGATGCACAGCCAGCAACCAAGGTG	705
DB	366	ACCTGGGGACCCAGACACCTACATCTGCGAACCCTGATGCACAGCCAGCAACCAAGGTG	425
QY	706	GACCAAGAAAGTTGACGCCCAATCTTGTCGCAAACTCACACAT	748
DB	426	GACCAAGAGTTGACGCCCAATCTTGTCGCAAACTCACACAT	468
RESULT	6		
AN403588			
LOCUS	AM403588	475 bp	mRNA
DEFINITION	UI-HF-BK0-abg-a-10-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone		EST 16-FEB-2000
ACCESSION	IMAGE:3056154	5', mRNA sequence.	
VERSION	AM403588		
KEYWORDS	AM403588.1	GI:6922573	
SOURCE	EST.		
ORGANISM	human.		
	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 475)		
JOURNAL	NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/ .		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Tel: (301) 496-1550		
	Email: Robert.Strausberg@nih.gov		
	Eco RI site shown at the beginning of the sequence.		
	Tissue Procurement: Louis M. Staudt, M.D., Ph.D.		
	cDNA Library Preparation: M.B. Soares Lab		
	cDNA Library Arrayed by: M.B. Soares Lab		
	DNA Sequencing by: M.B. Soares Lab		
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNI at: www.bio.lnlnl.gov/bbrp/image/image.html		
	Seq primer: M13 Forward		
FEATURES	Location/Qualifiers		
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	/db_xref="taxon:9606"		
	/clone="IMAGE:3056154"		
	/clone_lib="NIH_MGC_36"		
	/tissue_type="lymph"		
	/cell_type="germinal center B cells"		
	/cell_line="MGC85"		
	/lab_host="DH10B (lri)"		
	/note="vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."		
BASE COUNT	101 a 179 c 116 g 79 t		
ORIGIN			
Query Match	46.2%; Score 346.4; DB 72; Length 475;		
Best Local Similarity	94.5%; Pred. No. 8.7e-88;		
Matches 359; Conservative	0; Mismatches 21; Indels 0; Gaps 0;		
QY	369	CCCGAATTGGATATTTTGTATGTTGGGGGTCAAGAAACCTGTCTACTGTCTGACGCCCTC	428
DB	1	CACGAGGGGCTTCATGACAGTCTGGGGGCAAAAGGACACGCTCACCGTCTCTCAGCCTC	60
QY	429	CACCAAGGGCCCATGGGTCTCCCGCTGGCGGCTCTCCAGAGACACTCTGGGGGAC	488
DB	61	CACCAAGGGCCCATGGGTCTCCCGCTGGCGGCTCTCCAGAGACACTCTGGGGGAC	120
QY	489	AGCGGCGCTGGGCTCTGTCGTAAGACTACTTCCCGAACCAGGTGACGGTCTGCGAA	548
DB	121	AGCGGCGCTGGGCTCTGTCGTAAGACTACTTCCCGAACCAGGTGACGGTCTGCGAA	180
QY	549	CTCAGGCGCCTGACCAAGCGGCTGACACACTTCCCGGCTGTCTTACAGTCTCAGGACT	608

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Db 181 CTCAGGCGCCCTGACAGCGGGGTGCACACCTTCCGGCTGTCTACAGTCTCAGGACT 240
QY 609 CTACTCCCTCAGCAGGCGGTGGTACCGTCCCTCCAGCAGTCTGGGACCCAGACCTACAT 668
Db 241 CTACTCCCTCAGCAGGCGGTGGTACCGTCCCTCCAGCAGTCTGGGACCCAGACCTACAT 300
QY 669 CTGCAACGTGAATCAAGCCAGCAACACCAAGGTGGACAAAGATTGAGCCCAATC 728
Db 301 CTGCAACGTGAATCAAGCCAGCAACACCAAGGTGGACAAAGATTGAGCCCAATC 360
QY 729 TTGTGACAAAACCTCACACAT 748
Db 361 TTGTGACAAAACCTCACACAT 380

RESULT 7
LOCUS AW606291 566 bp mRNA EST 23-MAR-2000
DEFINITION QV0-HT0366-270100-087-a02 HT0366 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW606291
VERSION AW606291.1 GI:7311032
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 566)
AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT On Jun 15, 1998 this sequence version replaced gi:3224227.
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV0&t2=QV0-HT0366-270100-087-a02&t3=2000-01-27&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 21
High quality sequence stop: 566.
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/db_xref="taxon:9606"
/clone_lib="HT0366"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 117 a 188 c 151 g 110 t
ORIGIN
Query Match 45.8%; Score 343.8; DB 74; Length 566;
Best Local Similarity 79.2%; Pred. No. 4.9e-87;
Matches 408; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

QY 185 AGGCGCTGGAATGATGGGTGAGATCTTACCGGCTGTGGTAGCACCAGAAATATACCGAAA 244
Db 51 AGTGGATGGGATGGCTCAGTCTTTATGAAGCGGCACACAGACAACGCACACTACTCAGACA 110
QY 245 ATTTTAAAGACCGTGTACTATGACGGGTGACACTTCGACTAGTACATATACATGGAGC 304

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Db 111 GTTTCCAGCAGAGTACCATAACCGGGACAGTTCACAGCCACAGCCTACATGGAAT 170
QY 305 TCCTCCAGCGCTCGGATCGGAGGACACGCGCTCTATTATTGGCGCGTTATTTTGGTT 364
Db 171 TGAGGAGCCCTAAATCTGACGACACGCGCTCTATTATTGTGTGAGAGACGTCCTCCGTA 230
QY 365 CTAGCCCGGAATTGTTATTTGATGTTTGGGTCAAGGAACCTCTGCTCACTCTCTCGAGCG 424
Db 231 ATAGTAGTGGCTGCACCTCTCGCATTTGGGCCAGGGAACCTCTGTCATCTCTCTCTCAG 290
QY 425 CCTCCACAAAGGGCCCATCGGTCTTCCCGCTGGCGCCCTCTCTCCAAGAGCACCTCTTGGGG 484
Db 291 CCTCCACAAAGGGCCCATCGGTCTTCCCGCTGGCACCTCTCTCCAAGAGCACCTCTTGGGG 350
QY 485 GCACAGGGCCCTGGGCTGGCTGCTCAAGGACTACTTCCCGGAACCGGTGACGGTGTCTGT 544
Db 351 GCACAGGGCCCTGGGCTGGCTGCTCAAGGACTACTTCCCGGAACCGGTGACGGTGTCTGT 410
QY 545 GGAACCTCAGGCGCCCTGACACAGCGCGTGCACACCTTCCCGCTGTCTCTACAGTCTCTCAG 604
Db 411 GGAACCTCAGGCGCCCTGACACAGCGCGTGCACACCTTCCCGCTGTCTCTACAGTCTCTCAG 470
QY 605 GACTCTACTCTCTCAGCAGCGTGTGACCGCTGCCTCTCCAGCAGCTTGGGCACCCAGACCT 664
Db 471 GACTCTACTCTCTCAGCAGCGTGTGACCGTGCCTCTCCAGCAGCTTGGGCACCCAGACCT 530
QY 665 ACATCTGCAACGTGAATCAACAAGCCACACACACC 699
Db 531 ACATCTGCAACGTGAATCAACAAGCCACACACACC 565

RESULT 8
LOCUS AW402051 527 bp mRNA EST 16-FEB-2000
DEFINITION UT-HF-BKO-asg-c-05-0-UT.r1 NIH_MGC_36 Homo sapiens cDNA clone
IMAGE:3054345 5', mRNA sequence.
ACCESSION AW402051
VERSION AW402051.1 GI:6920737
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 527)
AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Feb 24, 1999 this sequence version replaced gi:4058273.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert\_Strausberg@nih.gov
ECO RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
FEATURES
source
1..527
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:3054345"
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/tissue_type="lymph"
/cell_type="germinal center B cells"
/lab_host="DH10B (LTI)"
/note="Vector: pMT3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA"

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High quality sequence start: 7
High quality sequence stop: 633.
Location/Qualifiers
1..634
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/db_xref="taxon:9606"
/clone_lib="HT0366"
/dev_stage="Adult"
/note="Organ: head,neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 130 a 172 c 193 g 139 t
ORIGIN

Query Match 44.5%; Score 333.6; DB 74; Length 634;
Best Local Similarity 74.28; Pred. No. 4e-84;
Matches 451; Conservative 0; Mismatches 149; Indels 8; Gaps 2;
QY 95 AGCCAGGGCCTCAGTCAAGTGTCTCTAAAGCTAGCGGCTATATTTTCTAATTAT 154
Db 609 AGCCCGCAAGTCTCTGAGACTCTCTCTGAAGCCTCTGGAATCAGTTCGACGATTATG 550
QY 155 GGATTCATAGTGGTGGTCAAGCCCGGCGAGGCGCTGGATGGATGGTGGATCTTAC 214
Db 549 CCATGCATGTGGTCCGGCAAGCTCCAGGAAGGGCGCTGGAGTGGTCTCAGTATCACTT 490
QY 215 CGGCTCTGTGAGCAGCAATATACCGAAATTTTAAAGCGTGTACTATGACCGTG 274
Db 489 GGAATAGTGAATGAAGACTATGGGACTCTGTGAAGGGCGGATTCACATCTCCAGAG 430
QY 275 ACATTCGACTAGTACAGTATACATGAGTCTCCAGGCTCGGATCGGAGGACAGCGCG 334
Db 429 ACACGTCAGAACTCCCTATATCTACAGTTGAACAGTCTGAGATTGAGACAGCGCT 370
QY 335 TCTATTATGCGCGGTTATTTTGTGTTCTAGCCCGAATGG-----TATTTTATG 388
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QY 389 TTTGGGTCAGGAACCTGTCTACGTCTCGAGCGCTCCACCAAGGCGCCATCGGTCT 448
Db 309 TCTGGGCGAGGACCAATGTCACCGTCTCTACGCTCCACCAAGGCGCCATCGGTCT 250
QY 449 TCCCGCTGGCGCCCTCCCTCAAGAGCAGCTCTGGGGGACAGCGCGCTCGGCTCGCTGG 508
Db 249 TCCAGCTGGCAGCCCTCCCTCAAGACAGCTCTGGGGGACAGCGCGCTCGGCTCGCTGG 190
QY 509 TCAAGGACTACTTCCCGAAGCGGTGACGGTGTCTGTGAAGTCAAGCGCCCTGACAGCG 568
Db 189 TCAAGGACTACTTCCCGAAGCGGTGACGGTGTCTGTGAAGTCAAGCGCGCTGACAGCG 130
QY 569 GCGTGCACACCTTCCCGGCTGTCTACAGTCTCTAGGACTCTACTCCCTCAGCAGCGTGG 628
Db 129 GCGTGCACACCTTCCCGGCTGTCTACAGTCTCTAGGACTCTACTCCCTCAGCAGCGTGG 70
QY 629 TGACCGTCCCTCCAGCAGTCTGGGACCCAGACCTACATCTGCAACGTGAATCAACAAG 688
Db 69 TGACCGTCCCTCCAGCAGTCTGGGACCC--AACCTACATCTGCAACGTGAATCAACAAC 12
QY 689 CCAGCAAC 696
Db 11 CAACAACC 4

RESULT 11
AW606325
LOCUS
DEFINITION QV0-HT0366-280100-088-509_1 HT0366 Homo sapiens cDNA, mRNA
455 bp mRNA EST 23-MAR-2000
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AW606325
AW606325.1 GI:7311066
EST.
human.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 455)
HCGP <http://www.ludwig.org.br/ORESTES>.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
On May 7, 1998 this sequence version replaced gi:3118791.
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?ci=QV0&t2=QV0-HT0366-280100-088-b09-1&t3=2000-01-28&t4=1>)
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High quality sequence stop: 455.
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/clone_lib="HT0366"
/dev_stage="Adult"
/note="Organ: head,neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 94 a 155 c 116 g 90 t
ORIGIN

Query Match
Best Local Similarity
Matches 362; Conservative 0; Mismatches 36; Indels 1; Gaps 1;

QY 351 TTATTTTGTGTTCTAGCCGGAATTTGGTATTTTGTATTTTGGGTCAAGGAACCTGGT 410
Db 11 TTATTTGTTCTGTGGTGTCCCTGCTCTGATATCTTGTATATCTGGGGCCAGGACAATGGT 70
QY 411 CACTGTCTCAGCGCTCCACCAAGGGCCCATCGGTCTTCCCTCGGCGCTCTCCCAAC 470
Db 71 CAACGTCTCTCAGCTCCACCAAGGGCCCATCGGTCTTCCCTCGGCGCTCTCCCAAC 130
QY 471 GAGCAGCTCTGGGGGACAGCGCCCTGGCTGCTTGGTCAAGGACTACTTCCCGAACC 530
Db 131 GAGCAGCTCTCGAGAGACAGCGCCCTGGCTGCTTGGTCAAGGACTACTTCCCGAACC 190
QY 531 GGTGAGCGGTCTCTGGAACCTCAGCGCCCTGACACAGCGGTGCACACCTTCCCGGTGT 590
Db 191 GGTGAGCGGTCTCTGGAACCTCAGCGCTCTGACAGCGGTGCACACCTTCCCGGTGT 250
QY 591 CCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGGTGGTGGACCGTCCCTCCAGCAGCTT 650
Db 251 CCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGGTGGTGGACCGTCCCTCCAGCAGCTT 310
QY 651 GGGCAGCCAGCCTACATCTGCAACGTGAATCAC--RAGCCAGCAGCACACCAAGTGGACA 709
Db 311 GGGCAGCCAGCCTACATCTGCAACGTGAATCAC--RAGCCAGCAGCACACCAAGTGGACA 370
QY 710 AGAAAGTTGAGCCCAATCTTGTGACAAAACCTCACACAT 748
Db 11

Db	371	AGAGAGTGGAGCCCAAAATCTTGTGCAGCAAAACACACACAT	409
RESULT	12		
LOCUS	AM403670		
DEFINITION	UI-HF-BK0-abh-b-03-0-ui.r1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3056189 5', mRNA sequence.		
VERSION	AM403670		
KEYWORDS	AM403670.1 GI:6922678		
SOURCE	EST.		
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert.Strausberg@nih.gov Eco RI site shown at the beginning of the sequence. Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: M.B. Soares Lab cDNA Library Arrayed by: M.B. Soares Lab DNA Sequencing by: M.B. Soares Lab Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/dbip/image/image.html Seq primer: M13 Forward.		
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	/cell_line="MGC85"		
	/lab_host="DH10B (LTI)"		
	/note="vector: p1773-Pac; Site_1: NotI; Site_2: Eco RI; constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."		
PAGE COUNT	121 a	207 c	150 g
ORIGIN			101 t

Query Match	42.9%	Score 322	DB 722	Length 579
Best Local Similarity	81.7%	Pred. No. 7,5e-81		
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				Gaps 2
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DB 10	GACAGTCCATTAACACCCGCCCTACCTGCAGTGTGAGCAGCCTTAAGGCCCTGGACACCCGC	69		
QY 334	GTCATATATGCGCGCGTATATTTTGTGGTTCTACGCCCAAT-----TGG	378		
DB 70	ATGTTATTCGTGGCAGACATGGGTTCCAGATTGTAGTATGACCAAGTCGTATGGGTGG	129		
QY 379	TATTTTGATGTTGGGGGTCAAGAAACCTGTGTCACTGTCTGAGGCGCTCCACCAAGGCG	438		
DB 130	TGGTTCGACCCCTGGGGCCAGGGAACCCGTGTACCGCTCTCTCAAGCTCCACCAAGGCG	189		
QY 439	CCATGGGTCCTCCCGCTGGCGCCCTCTCTCAAGAGCAGCTCTGGGGGGCACAGCGGCGCTG	498		
DB 190	CCATGGGTCCTCCCGCTGGCGCCCTCTCTCAAGAGCAGCCTCTGGGGGGCACAGCGGCGCTG	249		
QY 499	GGCTCCCTGGTCAAGAGCATCTTCCCGCAACCGGTGACGCTTCGTGGGAACCTCAGGCGCG	558		
DB 230	GGCTCCCTGGTCAAGAGCATCTTCCCGCAACCGGTGACGCTTCGTGGGAACCTCAGGCGCG	309		

QY	559	CTGACGAGGGGGTGTCTACACACCTTCCCGGGTGTCTCTACACTCCCTCAGAGACTCTTACTCTC	618
Db	310	CTGACGAGGGGGTGTCTACACACCTTCCCGGGTGTCTCTACAGTCTCTCAGAGACTCTTACTCTC	369
QY	619	AGCAGCGTGTGTACCGGTGCGCTTCCTCAGACAGCTTGGGCGCCAGACCTACATCTTGCAACGTG	678
Db	370	AGCAGCGTGTGTACCGGTGCGCTTCCTCAGACAGCTTGGGCGCCAGACCTACAGCTTCAACGTG	429
QY	679	AATCAAGCCCGACGACACCAAGGTGAGCAGAAAGTTGAGGCCCAATC-----TTGT	732
Db	430	AATCAAGCCCGACGACACCAAGGTGAGCAGAAAGTTGAGGCCCAATC-----TTGT	489
QY	733	GACAAACTCTACACAT	748
Db	490	GACACACTCTACACAT	505
RESULT	13		
LOCUS	AM375944/c		
DEFINITION	AM375944	442 bp	mRNA
ACCESSION	AM375944		
VERSION	AM375944.1	GI:6880598	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	human sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
TITLE	HCGP http://www.ludwig.org.br/ORESTES .		
JOURNAL	The FAPESP/LICR Human Cancer Genome Project		
COMMENT	Unpublished (1999)		
	On Jul 8, 1999 this sequence version replaced gi:5422592.		

Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel.: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC2&t2=RC0-CT0201>
 270999-011-e04&t3=1999-09-27&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 9
 High quality sequence stop: 442.
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 /db_xref="taxon:9606"
 /clone_lib="CT0201"
 /dev_stage="Adult"
 /note="Organ: colon; Vector: puc18; Site.1: Sma1; Site.2:
 Sma1; A mini-library was made by cloning products derived
 from ORESTES PCR (U.S. Letters Patent application No.
 196,716 - Ludwig Institute for Cancer Research) profiles
 into the pUC 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."
 BASE COUNT 78 a 106 c 166 g 92 t
 ORIGIN
 Query Match 42.8%; Score 320.8; DB 71; Length 442;
 Best Local Similarity 99.4%; Pred. No. 1.5e-80;
 Matches 322; Conservative 0; Mismatches 2; Indels 0; Gaps 0.
 425 CCTCACAAGAGGGCCCATGGTCTTCCCTTGCGCCCTCTCTCAAGAGACACTCTGGGG 484
 |||||
 DB 442 CCTCACAAGAGGGCCCATGGTCTTCCCTTGCGCCCTCTCTCAAGAGACACTCTGGGG 383

BASE COUNT 92 a 160 c 118 g 76 t
ORIGIN

Query Match 42.5%; Score 318.6; DB 72; Length 446;
Best Local Similarity 88.3%; Pred. No. 6.5e-80;
Matches 361; Conservative 0; Mismatches 39; Indels 9; Gaps 1;

QY 320 CGGAGACACGGCCGCTATTATTGGCCGTTATTTTTTGGTTCTAGCCCGAATTGGT 379
Db 8 CTGACGACACGGCCGATATTACTGTCCAGAGAACTTCCAGTGGCTGSCC----- 58

QY 380 ATTTGATCTTTGGGTCAAGGAACCTTGGTCACTGTCTCGAGCGCTCCACCAAGGGCC 439
Db 59 ACCATGACTACTTGGGCCAGGGAACCTTGGTCACTGTCTCGAGCTTCCACCAAGGGCC 118

QY 440 CATCGGTCTTCCCGTGGCGCCCTCTCCAAAGACACCTCTGGGGGCACAGGGCCCTGG 499
Db 119 CATCGGTCTTCCCGTGGCGCCCTCTCCAGGAGCACCTCTGGGGGCACAGGGCCCTGG 178

QY 500 GCTGCTGTCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGGAACCTCAGGGGCC 559
Db 179 GTTGTCTGTCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGGAACCTCAGGGGCC 238

QY 560 TGACGAGCGCGGTGCACACCTTCCCGGCTGTCTACAGTCCCTCAGGACTCTTACCTCC 619
Db 239 TGACGAGCGCGGTGCACACCTTCCCGGCTGTCTACAGTCCCTCAGGACTCTTACCTCC 298

QY 620 GCAGGTGTGTGACCGTGCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAAGTGA 679
Db 299 GCATGTGTGTGACCGTGCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAAGTGA 358

QY 680 ATCAAGCCCCAGCACACCAAGGTGGACAAGAAAGTTGAGCCCAATC 728
Db 359 ATCAAGCCCCAGCACACCAAGGTGGACAAGAAAGTTGAGCTCAAAAC 407

Search completed: September 12, 2000, 20:04:56
Job time: 3493 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 12, 2000, 21:01:09 ; Search time 73.77 Seconds

(without alignments)
2543.636 Million cell updates/sec

Title: US-08-487-283a-12

Perfect score: 750

Sequence: 1 ATGAAGTGGAGCTGGGTAT.....GTGACAAACTGCACATCA 750

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 311585 segs, 125096042 residues

Total number of hits satisfying chosen parameters: 623170

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	750	100.0	750	1	T08484
2	737.2	98.3	750	1	T08487
3	729.2	97.2	750	1	T08483
4	561.2	74.8	750	1	T08482
5	494	65.9	2071	1	V70080
6	490.4	65.4	8120	1	V44856
7	489.2	65.2	2077	1	V70079
8	488	65.1	901	1	V55073
9	488	65.1	927	1	V55072
10	488	65.1	6563	1	V44953
11	487.8	65.0	1449	1	X06951
12	487.8	65.0	1449	1	X06952
13	478.2	63.8	1617	1	Q35099
14	476	63.5	9208	1	O65629
15	476	63.5	19001	1	V61793
16	472.8	63.0	6072	1	V71265
17	471.2	62.8	6072	1	V63493
18	467.4	62.3	3282	1	T40914
19	467.4	62.3	13254	1	T40915
20	462.4	61.7	1493	1	X07423
21	462.4	61.7	2143	1	X03840
22	459.6	61.3	762	1	T03381
23	459.6	61.3	762	1	T03395
24	459.6	61.3	762	1	T93550
25	459.6	61.3	762	1	V03427
26	459.6	61.3	762	1	V06418
27	459.6	61.3	762	1	V10317
28	459.6	61.3	762	1	V44852
29	458.2	61.1	1382	1	T62936
30	454.8	60.6	1395	1	V62935
31	453.8	60.3	2178	1	V81689
32	452.2	60.3	2178	1	O25592
33	445.6	59.4	3400	1	T62937

34	445.6	59.4	5300	1	T62938
35	443.2	59.1	687	1	T15202
36	443.2	59.1	4691	1	O92546
37	443.2	59.1	6166	1	O92547
38	442.2	59.0	6557	1	T15932
39	434.4	57.9	11529	1	Q43844
40	432.8	57.7	756	1	T03364
41	432.8	57.7	756	1	T78571
42	432.8	57.7	756	1	T93546
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ALIGNMENTS

RESULT 1
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ID T08484 standard; DNA; 750 BP.
AC T08484:
DT 02-APR-1996 (first entry)
DE Humanised 5G1.1 VH + IGHRLC DNA.
KW Complement C5; haemolysis; kidney; glomerulonephritis;
KW monoclonal antibody; antineoplastic; antibody engineering;
KW humanised antibody; complementarity determining region; CDR;
KW ds.
OS Synthetic.
FH Key
FT cds
FT 1..750
FT /tag- a
FT signal_peptide 1..57
FT /tag- b
FT mat_peptide 58..747
FT /tag- c

FN W09529697-A1.
PD 09-NOV-1995.
PF 01-MAY-1995: U05688.
PR 02-MAY-1994: US-236208.
PA (ALEX-) ALEXON PHARM INC.
PI Evans MJ, Matlis L, Mueller EE, Rollins S;
PI Roher RP, Spinghorn J P, Squinto SP, Thomas TC;
PI Wang Y, Wilkins JA.
DR WPI: 95-392923/50.
DR P-PSDB: R77611.
PT Treating glomerulonephritis with antibody against complement C5
PT component - to inhibit complement induced cell lysis
PS Claim 38: Page 123-125; 18pp; English.
CC A DNA construct (T08483) codes for a humanised CDR-grafted and
CC framework sequence-altered fd 5G1.1 VH + IGHRL (R77610), which
CC includes CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1.
CC The DNA can be subcloned together with DNA (T08484) coding for a
CC humanised light chain (R77612) into vector APEX-3P (T08476) for
CC expression of humanised antibody in human 293 EBNA cells. Such
CC recombinant antibodies retain the ability of Mab 5G1.1 to block
CC human complement C5a generation and thus to reduce glomerular
CC inflammation and kidney dysfunction associated with
CC glomerulonephritis.
SQ Sequence 750 BP; 163 A; 220 C; 197 G; 170 T;

Query Match 100.0%; Score 750; DB 1; Length 750;
Best Local Similarity 100.0%; Pred. No. 1.8e-177;
Matches 750; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGAAGTGGAGCTGGGTATCTCTCTCTCTGTAAGTAACTGGGGGTCACTCCAA 60
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Qy	181	GGCAGGGCCCTGGAATGGATGGGTGAGATCTTACCGGGCTCTGGTAGCACCGCAATATACC	240
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Qy	241	GAATAATTTAAAGACCGGTGTTACTATGACGGCTGACACTTCGACTAGTACATATACATG	300
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Qy	301	GAGCTCTCCAGCGCTGGATCGGAGGACAGGGCGCTCTATTATTCGCGGTTATTTTTT	360
Db	301	GAGCTCTCCAGCGCTGGATCGGAGGACAGGGCGCTCTATTATTCGCGGTTATTTTTT	360
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Qy	541	TCGTGGAACTCAGCGGCCCTTGACAGCGGGCTGCACACCTTCCCGGCTCTCTCAGATCC	600
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Qy	661	ACCTTACATCTGCAACGTGAATCAAGCCCCAGCAACCAAGGTGACAAAGAAAGTTGAG	720
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Qy	721	CCCAAAATCTGTGACAAAACCTACACATAA	750
Db	721	CCCAAAATCTGTGACAAAACCTACACATAA	750

RESULT 2

ID	T08487 standard; DNA; 750 BP.
AC	T08487;
DT	02-APR-1996 (first entry)
DE	Humanised 5G1.1 VH + IGHRLD DNA.
KW	Complement C5; haemolysis; kidney; glomerulonephritis;
KW	monoclonal antibody; antiinflammatory; antibody engineering;
KW	humanised antibody; complementarity determining region; CDR;
ds.	
OS	Synthetic.
FH	Key
FT	cds
FT	1. .750
FT	/*tag= a
FT	signal_peptide 1. .57
FT	/*tag= b
FT	mat_peptide 58. .747
FT	/*tag= c
PN	W09529697-A1.
PD	09-NOV-1995.
PF	01-MAY-1995; U05688.
PR	02-MAY-1994; US-236208.
PA	(ALEX-) ALEXION PHARM INC.
PI	Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S;
PI	Rother RP, Springhorn J P, Squinto SP, Thomas TC;
PI	Wang Y, Wilkins JA;
DR	WPI; 95-392923/50.
DR	P-PSDB: R77615.

Best Local Similarity 81.5%; Pred. No. 7.7e-114; Matches 585; Conservative 0; Mismatches 130; Indels 3; Gaps 1;

QY 1 ATGAAGTGGAGTGGATTTCTCTCCCTGTCAGTAACTGCGGGGCTCCAGTCCCA 60
 DB 21 ATGGATGGAGTGGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 80
 QY 61 GTCCAACTGGTCAATCCGGCCGAGGTCAAGAACGAGGGGCTTCAGTCAAGTTC 120
 DB 81 GTCCAACTGGTCAATCCGGCCGAGGTCAAGAACGAGGGGCTTCAGTCAAGTTC 140
 QY 121 TGTAAAGTACGGCTATATTTTCTTAATTAATTTGATTCAGTGGGCTGAGGCCCC 180
 DB 141 TGCAGAGGCTTGTGGTCAACCTTCACCGACTGATGCACTGGGTAAAGAGGCCCC 200
 QY 181 GGGGAGGCGCTGGAATGGATGGGATCTTACCGGGGCTGGTGAAGCAGGAATATAC 240
 DB 201 GGACAGGCGCTTGAATGGATGGGATGGGATGGGATGGGATGGGATGGGATGG 260
 QY 241 GAAATTTTAAAGACCTGTTACTATGACGCGTACACTTCCAGTACAGTATACATG 300
 DB 261 CAAAGTTCAGAGGGGACGACATGATGACATGACATGACATGACATGACATGAC 320
 QY 301 GAGCTCTCAGCTGCGATCGGAGACAGGCGGCTATATTTGCGCGCTATTTT 360
 DB 321 GAGCTCAGCAGCTGAGATCTGAGGACAGGCGGCTATATTTGCGCAAGAA--TAG 377
 QY 361 GGTCTAGCGCGAATTTGATTTGTTGGGTCAGAAACCTGCTACTGCTG 420
 DB 378 GACTATATTAACACTGTTACTTCTGATGCTGAGGAGGAGGAGGAGGAGGAGG 437
 QY 421 AGGCGCTCCACCAAGGGGCGCATCGCTTCCCTCGGCGCTCTCCAGAGCACTCT 480
 DB 438 TCAGCTCCACCAAGGGGCGCATCGCTTCCCTCGGCGCTCTCCAGAGCACTCT 497
 QY 481 GGGGCGACAGCGGCGCTGCGCTGCTGCTCAAGACTACTTCCCGAAGCGGTGAG 540
 DB 498 GGGGCGACAGCGGCGCTGCGCTGCTGCTCAAGACTACTTCCCGAAGCGGTGAG 557
 QY 541 TCGTGGAACTAGAGGGGCGCTGACAGCGGCGCTGACACCTTCCGGCTCTCTACAG 600
 DB 558 TCGTGGAACTAGAGGGGCGCTGACAGCGGCGCTGACACCTTCCGGCTCTCTACAG 617
 QY 601 TCAGGACTCTACTCCTCTCAGCAGCTGATGACGCTGCTCCAGAGCTTGGGACCCG 660
 DB 618 TCAGGACTCTACTCCTCTCAGCAGCTGATGACGCTGCTCCAGAGCTTGGGACCCG 677
 QY 661 ACCTACATCTGCAACGATCAATCAAGCCCAAGCAACCAAGGAGTGAAGAGTTG 718
 DB 678 ACCTACATCTGCAACGATCAATCAAGCCCAAGCAACCAAGGAGTGAAGAGTTG 735
 RESULT 6
 ID V44956
 AC V44956
 DE 15-FEB-1999 (first entry)
 KW Humanised anti-body plasmid p6G4V11N35A.chosd.9.
 KW Humanised anti-body plasmid p6G4V11N35A.chosd.9.
 KW Human: Fcb: Interleukin-8; inflammation; immunotherapy; psoriasis;
 KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KW ischaemic reperfusion; adult respiratory distress syndrome;
 KW dermatitis; meningitis; encephalitis; uveitis; autoimmune disease;
 KW rheumatoid arthritis; Sjogren's syndrome; vasculitis;
 KW leukocyte diapedesis; multiple organ injury syndrome; septicemia;
 KW trauma; alcoholic hepatitis; pneumonia; pleurisy; alveolitis;
 KW vasculitis; bronchiectasis; bronchiectasis; cystic fibrosis; diagnosis;
 KW therapy; p6G4V11N35A.chosd.9; ds; cyclic; circular.
 OS Chimeric - Mus sp.
 OS Chimeric - Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 1363..2721
 FT /*tag- a

PN W09637200-A2.
 PD 27-AUG-1998.
 PE 20-FEB-1998; U03337.
 PR 22-JAN-1998; US-012116.
 PR 21-FEB-1997; US-804444.
 PA (GETH) GENENTECH INC.
 PI Hsai V, Koumenis I, Leong SR, Presta LR, Shahrokh Z,
 PI Zapata GA;
 DR WPI: 98-467563/40.
 DR P-PDB: W69316.
 PT New conjugates of antibody fragments - having covalently attached
 PT non-proteinaceous polymer molecules, particularly polyethylene
 PT glycol, for improving the residence time in the circulation.
 PS Example P: Fig 48A-Z; 328bp; English.
 CC This is the DNA sequence of vector plasmid p6G4V11N35A.chosd.9
 CC encoding a humanised 6G4V11N35A IgG (see W69316) containing
 CC complementarity determining regions of murine anti-interleukin-8
 CC (IL-8) monoclonal antibody (Mab) 6G5.2.5 (see W69309-10) in a
 CC human template. The plasmid has a pSV1 backbone. Humanised
 CC anti-IL-8 Mabs (see W69301-04) are described for use in diagnostic
 CC applications and in the treatment of inflammatory disorders. The
 CC invention provides conjugates of an antibody fragment and a
 CC polymer, such as PEG, that have improved half-life, mean residence
 CC time, and/or clearance rate. The conjugates can be used for immune
 CC therapy of e.g. psoriasis, responses associated with inflammatory
 CC bowel disease (such as Crohn's disease and ulcerative colitis),
 CC ischaemic reperfusion, adult respiratory distress syndrome,
 CC dermatitis, meningitis, encephalitis, uveitis, autoimmune diseases
 CC such as rheumatoid arthritis, Sjogren's syndrome, vasculitis,
 CC diseases involving leukocyte diapedesis, central nervous system
 CC inflammatory disorder, multiple organ injury syndrome secondary to
 CC septicemia or trauma, alcoholic hepatitis, bacterial pneumonia,
 CC antigen-antibody complex mediated diseases, inflammations of the
 CC lung, including pleurisy, alveolitis, vasculitis, pneumonia,
 CC chronic bronchitis, bronchiectasis, and cystic fibrosis.
 SQ Sequence 8120 BP; 2023 A; 2182 C; 1958 G; 1957 T;

Query Match 65.4%; Score 490.4; DB 1; Length 8120;

Best Local Similarity 78.5%; Pred. No. 8.5e-113; Matches 587; Conservative 0; Mismatches 161; Indels 0; Gaps 0;

QY 1 ATGAAGTGGAGTGGATTTCTCTCCCTGTCAGTAACTGCGGGGCTCCAGTCCCA 60
 DB 1306 ATGGATGGAGTGGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1365
 QY 61 GTCCAACTGGTCAATCCGGCCGAGGTCAAGAACGAGGGGCTTCAGTCAAGTTC 120
 DB 1366 GTTCAGCTAGTGAAGTGGGCTGGGCTGCTGACAGAGGGGCTTCCGTTGTCC 1425
 QY 121 TGTAAAGTACGGCTATATTTTCTTAATTAATTTGATTCAGTGGGCTGAGGCCCC 180
 DB 1426 TGTGAGCTTGTGGTCAACCTTCACCGACTGATGCACTAGTACGCTGCTCAGGCCCC 1485
 QY 181 GGGGAGGCGCTGGAATGGATGGGATCTTACCGGGGCTGGTGAAGCAGGAATATAC 240
 DB 1486 GGTAAAGGCGCTGGAATGGATGGGATGGGATGGGATGGGATGGGATGGGATGG 240
 QY 241 GAAATTTTAAAGACCTGTTACTATGACGCGTACACTTCCAGTACAGTATACATG 300
 DB 1546 CAAAGTTCAGAGGGGCGCTTCACTTATCTCGGCAACCTCCAAAACACAGATACCTG 1605
 QY 301 GAGCTCTCAGCTGCGATCGGAGACAGCGGCTATATTTGCGCGGTTATTTT 360
 DB 1606 CAGATGAACAGCTGCGTGTGAGACACTGCGCTATATCTGCAAGAGGAGTAT 1665
 QY 361 GGTTCAGCGCGAATGATTTTGTGTTGGGTCAGAAAGAACTGCTACTGCTG 420
 DB 1666 CGCTCAATAGTGTATGTTGTTGCTGAGCTGCTGGGTCAGAAAGAACTGCTACTGCTG 1725
 QY 421 AGGCGCTCAGCAAGGGGCGCATGCGTCCCTCGGCGCGCTCCCAAGAGCACTCT 480
 DB 1726 TCGGCTCAGCAAGGGGCGCATGCGTCCCTCGGCGCGCTCCCAAGAGCACTCT 1785

RESULT 9

V55072 standard; DNA; 927 BP.
 AC V55072;
 DT 15-FEB-1999 (first entry)
 DE Humanised anti-IL-8 6G4.2.5V11N35A heavy chain DNA.
 KW Humanised antibody; monoclonal antibody; interleukin-8;
 KW 6G4.2.5; inflammation; immunotherapy; therapy; psoriasis;
 KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KW ischaemic reperfusion; adult respiratory distress syndrome;
 KW dermatitis; meningitis; encephalitis; uveitis; autoimmune disease;
 KW rheumatoid arthritis; Sjorgen's syndrome; vasculitis;
 KW leukocyte diapedesis; multiple organ injury syndrome; septicemia;
 KW trauma; alcoholic hepatitis; pneumonia; pleurisy; alveolitis;
 KW vasculitis; bronchitis; bronchiectasis; cystic fibrosis; diagnosis;
 ds.
 OS Chimeric - Homo sapiens.
 OS Chimeric - Mus sp.
 OS Synthetic.
 FH Key
 FT CDS Location/Qualifiers
 31..927
 /*tag= a
 FT sig_peptide 31..99
 /*tag= b
 /*note= "STII peptide leader"
 FT mat_peptide 100..924
 /*tag= c
 WO9837200-A2.
 PD 27-AUG-1998.
 PF 20-FEB-1998; U03337.
 PR 22-JAN-1998; US-012116.
 PR 21-FEB-1997; US-80444.
 PA (GETH) GENENTECH INC.
 PI Hsai V, Koumenis I, Leong SR, Presta LR, Shahrokh Z,
 PI Zapata GA;
 DR WPI; 98-467563/40.
 DR P-PSDB; W69303.
 PT New conjugates of antibody fragments - having covalently attached
 PT non-proteinaceous polymer molecules, particularly polyethylene
 PT glycol, for improving the residence time in the circulation.
 PS Disclosure; Fig 37; 32pp; English.
 CC This DNA sequence encodes humanised anti-interleukin-8 (IL-8)
 CC antibody 6G4.2.5V11N35A heavy chain (see W69303) in an N-terminal
 CC fusion with the STII leader peptide and in a C-terminal fusion
 CC with the GCN4 leucine zipper and which contains the complementarity
 CC determining regions (CDRs) of murine anti-IL-8 antibody 6G4.2.5
 CC heavy chain (see W69310) within a human IgG1 subgroup III heavy
 CC chain template. Humanised anti-IL-8 monoclonal antibodies (MAbs)
 CC and variants are described for use in diagnostic applications
 CC and in the treatment of inflammatory disorders. The invention
 CC provides conjugates of an antibody fragment and a non-proteinaceous
 CC polymer, such as PEG, that have improved half-life, mean residence
 CC time, and/or clearance rate compared to non-derivatised parental
 CC antibody fragment. Also claimed are a polypeptide that is an
 CC anti-IL-8 MAb or antibody fragment comprising a light chain amino
 CC acid sequence comprising the light chain CDRs of 6G4.2.5V11N35A (see
 CC W69301) or 6G4V11N35E (see W69302) and the heavy chain and leucine
 CC zipper of 6G4.2.5V11N35A, and a F(ab')2 antibody fragment comprising
 CC the heavy chain of 6G4.2.5V11N35A in which the Cys231 and Cys234
 CC residues form a disulphide linkage. The conjugates are used for
 CC immune therapy of inflammatory disorders, e.g. psoriasis, responses
 CC associated with inflammatory bowel disease (such as Crohn's disease
 CC and ulcerative colitis), ischemic reperfusion, adult respiratory
 CC distress syndrome, dermatitis, meningitis, encephalitis, uveitis,
 CC autoimmune diseases such as rheumatoid arthritis, Sjorgen's
 CC syndrome, vasculitis, diseases involving leukocyte diapedesis,
 CC central nervous system inflammatory disorder, multiple organ injury
 CC syndrome secondary to septicemia or trauma, alcoholic hepatitis,
 CC bacterial pneumonia, antigen-antibody complex mediated diseases,
 CC inflammations of the lung, including pleurisy, alveolitis,
 CC vasculitis, pneumonia, chronic bronchitis, bronchiectasis, and
 CC cystic fibrosis. They can also be used in diagnostic applications.
 CC Sequence 927 BP; 217 A; 268 C; 239 G; 203 T;

Query Match 65.1%; Score 488; DB 1; Length 927;
 Best Local Similarity 79.4%; Pred. No. 1.9e-112;
 Matches 578; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

QY	21	TCCTTCCTCCTGTCAGTAACTGCGCGCTCCACTCCCAAGTCCCAACTGCTGCAATCCGG	80
DB	63	TATGTTTCGTTTTTCTATTGCTACAAACGCTACGCTAGGTTTCAGTACGTAGTCTGG	122
QY	81	CGCGAGGTCACAGACCGCAGGCGCTCAGTCAAGTGTCTCTGTAAGCTAGCGGCTATAT	140
DB	123	CGGTGCGCTGGTGACACCGAGGCGCTCACTCCGTTTGTCTGTGTCAGCTTCTGCTACT	182
QY	141	TTTTCCTAATTAATGAGTCAATGCGTGGTTCAGGCGCGCGCGGCGAGGCTGGAATGGAT	200
DB	183	CTTCTCGAGTCACTATATGAGTGGTTCGTGAGGCGCGGCTGAGGCTGGAATGGGT	242
QY	201	GGTGAGATCTTACCGGCTCTGTGAGCACCGCAATATACCGAAATTTTAAAGACCGTGT	260
DB	243	TGGATATATTGATCCTTCCAATGTTGAACTACGTATATCAAAAGTTCAAGGCGCTTT	302
QY	261	TACTATGACCGGTGACACTTCGACTAGTACAGTATACATGAGAGCTCTCCAGCCTCGATC	320
DB	303	CACCTTATCTCGCGACAACTCCAAAACACAGCATACCTGCAGATGAACAGCCTGGGTGC	362
QY	321	GGAGGACACGGCGTCTATTATTGCGCGGTTATTTTGTGTTCTAGCCCGAATGGTA	380
DB	363	TGAGGACACTGCGCTCTATTACTGTCAAGAGGGGATTATCGCTACATGGTCTACGGTT	422
QY	381	TTTTGATGTTTGGGTCAAAGAACCTTGCTGCTGAGCGCTCCACCAAGGCGCC	440
DB	423	CTTCGAGCTCTGGGTCAGGAACCTTGCTCAGCGTCTCTCGGCTCCACCAAGGCGCC	482
QY	441	ATCGGTCTTCCCGCTGGCGCTCTCTCAAGAGACCTCTGGGGGACAGCGCCCTGGG	500
DB	483	ATCGGTCTTCCCGCTGGCACCTCTCTCAAGAGACCTCTGGGGGACAGCGCCCTGGG	542
QY	501	CTGCGTGGTCAAGGACTACTTCCCGAACCGGTGAGCGGTGCTGTGNACTCAGCGCCCT	560
DB	543	CTGCGTGGTCAAGGACTACTTCCCGAACCGGTGAGCGGTGCTGTGNACTCAGCGCCCT	602
QY	561	GACACGCGGTGCACACCTTCCCGGTGCTCTACAGTCTCTCAGGACTCTACTTCCCTCAG	620
DB	603	GACACGCGGTGCACACCTTCCCGGTGCTCTACAGTCTCTCAGGACTCTACTTCCCTCAG	662
QY	621	CAGCGTGGTACCGTCCCTCCAGAGCTTGGGACCCAGACCTACATCTGCAACGTAA	680
DB	663	CAGCGTGGTACCGTCCCTCCAGAGCTTGGGACCCAGACCTACATCTGCAACGTAA	722
QY	681	TCACAGCCCGACACACAGGTGGACAGAAAGTTGAGCCCAATCTTGTGACAAAC	740
DB	723	TCACAGCCCGACACACAGGTGGACAGAAAGTTGAGCCCAATCTTGTGACAAAC	782
QY	741	TCACACAT 748	
DB	783	TCACACAT 790	
RESULT	10		
V44953			
ID	V44953 standard; cDNA; 6563 BP.		
AC	V44953;		
DT	15-FEB-1999 (first entry)		
DE	Anti-IL-8 humanised antibody plasmid p6G4V11N35A.F(ab')2.		
KW	Humanised antibody; chimeric antibody; monoclonal antibody; mouse;		
KW	human; Fab; interleukin-8; inflammation; immunotherapy; psoriasis;		
KW	inflammatory bowel disease; Crohn's disease; ulcerative colitis;		
KW	ischaemic reperfusion; adult respiratory distress syndrome;		
KW	dermatitis; meningitis; encephalitis; uveitis; autoimmune disease;		
KW	rheumatoid arthritis; Sjorgen's syndrome; vasculitis;		
KW	leukocyte diapedesis; multiple organ injury syndrome; septicemia;		
KW	trauma; alcoholic hepatitis; pneumonia; pleurisy; alveolitis;		

QY 355 -----TTTTTGGTTCTAGCCGAATGGTATTTTGTATTTTGGGGTCAAGGAACC 405
 Db 395 AGCAGGCAATTTGACGGGCGCGGTGGCTGGTTCGACCCCTGGGGCCAGGGACC 454
 QY 406 CTGGTCACTGCTCGAGCGCTCCACCAAGGGCCATCGGCTTCCTCCCGCCCTCC 465
 Db 455 CTGGTCACTGCTCCTCAGCGCTCCACCAAGGGCCATCGGCTTCCTCCCGCCCTCC 514
 QY 466 TCCAAGAGCACTTGGGGGCACAGCGCCCTGGCTGGCTTCAGGACTACTTCC 525
 Db 515 TCCAAGAGCACTTGGGGGCACAGCGCCCTGGCTGGCTTCAGGACTACTTCC 574
 QY 526 GAACCGGTGACGGTGTGGTGAAGTCAAGCGCCCTGACACGCGGTGCACACCTTC 585
 Db 575 GAACCGGTGACGGTGTGGTGAAGTCAAGCGCCCTGACACGCGGTGCACACCTTC 634
 QY 586 GGTGCTCTACAGCTCTCAGGACTCTACTCCCTCAGCAGCGGTGGTACCGTCC 645
 Db 635 GCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGGTGGTACCGTCC 694
 QY 646 AGCTTGGGCAACCACTACATCTCAACGTGAATCACAAGCCCGACCAACCAAGTG 705
 Db 695 AGCTTGGGCAACCACTACATCTCAACGTGAATCACAAGCCCGACCAACCAAGTG 754
 QY 706 GACAAGAAAGTTGAGCCCAATCTTGACAAAATCTACACAT 748
 Db 755 GACAAGAAAGTTGAGCCCAATCTTGACAAAATCTACACAT 797

RESULT 14

Q65629
 ID Q65629 standard; DNA; 9208 BP.
 AC Q65629;
 DT 01-FEB-1995 (first entry)
 DE Vector contg. TCAE 8 DNA.
 KW B cell lymphoma chimeric antibody; CD20; peripheral blood cells;
 KW cell lysis; ss.
 OS Synthetic.
 PN W09411026-A.
 PD 26-MAY-1994.
 PF 12-NOV-1993; U10953.
 PR 13-NOV-1992; US-978891.
 PR 03-NOV-1993; US-149099.
 PA (IDEC-) IDEC PHARM CORP.
 PI Anderson DR, Hanna N, Leonard JE, Newman RA, Rastetter WH;
 PI Refine;
 DR WPI; 94-183162/22.
 PT Treating B cell lymphoma with chimeric antibody - against CD20,
 PT causing rapid depletion of peripheral B cells, also new
 PT antibodies and hybridomas
 PS Disclosure; Fig 3; 101pp; English.
 CC The sequence shows a vector contg. TCAE8, a gene encoding a chimeric
 CC anti-CD20 antibody for treatment of B cell lymphomas. TCAE8
 CC contains 4 transcriptional cassettes, human Ig light and heavy chain
 CC constant regions, dihydrofolate reductase, neomycin phosphotransferase
 CC and murine variable regions. The vector can be used to produce
 CC antibodies which cause depletion of peripheral blood B cells,
 CC including those associated with lymphoma. They mediate complement-
 CC dependent lysis and lyse target cells by antibody-dependent cellular
 CC cytotoxicity.
 CC See also Q65629-35.
 SQ Sequence 9208 BP; 2237 A; 2399 C; 2388 G; 2182 T;

Query Match 63.5%; Score 476; DB 1; Length 9208;
 Best Local Similarity 78.2%; Pred. No. 3.3e-109;
 Matches 585; Conservative 0; Mismatches 160; Indels 3; Gaps 1;

QY 1 ATGAAGTGGAGCTGGGTATTTCTTCTCTCTGTCAGTAAGTGGCGGTCCACATCCCAA 60
 Db 2400 ATGGGTTGGAGCCCTCATCTTCTCTCTCTGTCAGTACGCGTCTCTGTCGCCAG 2459

QY 61 GTCCAACCTGGTGCATCCGGCCGCGAGGTCAAGAAAGCAGGGCCCTCAGTCAAAGTGCC 120
 Db 2460 GTACAACCTGGTGCATCCGGCCGCGAGGTCAAGAAAGCAGGGCCCTCAGTCAAAGTGCC 2519
 QY 121 TGTAAAGCTAGCGGTATATTTTCTTAATTAATGGAATCAATGGGTGGGTGAGGCCCC 180
 Db 2520 TGTAAAGCTAGCGGTATATTTTCTTAATTAATGGAATCAATGGGTGGGTGAGGCCCC 2579
 QY 181 GGGCAGGCGCTGGGAATGGATGGTGGATCTTACCGGCTCTGGTAGCACCAATATACC 240
 Db 2580 GGTGGGCGCTGGGAATGGATGGAGCTATTTATCCGGAATGGTGGTACTTCTTCAAT 2639
 QY 241 GAAATTTTAAAGACCGGTACTATGACGCGTGACACTTCGACTAGTACATATACATG 300
 Db 2640 CAGAGTTCAAGGCAAGCCACATGACTGCAGACAAATCTCCAGCACACCTACATG 2699
 QY 301 GAGCTCTCCAGCGCTCGGATCGGAGACAGCGCGTCTATTATTGCGCGGTATTTT 360
 Db 2700 CAGCTCAGCAGCGCTGACATCTGAGGACTCTGCGGTCTATTACTGTCAAGATCGACT-- 2757
 QY 361 GGTCTACCGCAATGGTATTTTGTATTTGGGTCAAGGAACCTGGTCACTGTCTCG 420
 Db 2758 -ACTAGGCGGTGACTGGTACTTCAATGTCTGGGCGCAGGACACCGTCACTCT 2816
 QY 421 AGCGCTCCACCAAGGCGCCATCGGTCTTCCCGCTGGGCGCCCTCTCCCAAGAGCACTCT 480
 Db 2817 GCAGCTAGCACCAAGGCGCCATCGGTCTTCCCGCTGGCACCCTCTCCCAAGAGCACTCT 2876
 QY 481 GGGGCACAGCGCGCTGGGTGCTGCTGCTCAAGGACTACTTCCCGAACCGGTGAGGTTG 540
 Db 2877 GGGGCACAGCGCGCTGGGTGCTGCTGCTCAAGGACTACTTCCCGAACCGGTGAGGTTG 2936
 QY 541 TCGTGAACCTCAGCGCGCTGACAGCGCGGTGCACACCTTCCCGCTGTCTACAGTCC 600
 Db 2937 TCGTGAACCTCAGCGCGCTGACAGCGCGGTGCACACCTTCCCGCTGTCTACAGTCC 2996
 QY 601 TCAGGACTCTACTCTCAGCAGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 660
 Db 2997 TCAGGACTCTACTCTCAGCAGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 3056
 QY 661 ACCTACATCTGCAAGGTGAATCACAAGCCCGACCAACACCAAGGTGGACAAAGTTGAG 720
 Db 3057 ACCTACATCTGCAAGGTGAATCACAAGCCCGACCAACACCAAGGTGGACAAAGTTGAG 3116
 QY 721 CCCAATCTTGTGACAAAATCTACACAT 748
 Db 3117 CCCAATCTTGTGACAAAATCTACACAT 3144

RESULT 15

V61793
 ID V61793 standard; DNA; 19001 BP.
 AC V61793;
 DT 07-JUN-1999 (first entry)
 DE Traget plasmid Molly containing anti-CD20 gene.
 KW Molly; target plasmid; gene integration; gene amplification;
 KW homologous recombination; vector; neomycin phosphotransferase;
 KW neo gene; selectable marker; immunoglobulin; CD20; C2B8; human; ss.
 OS Chimeric - Mus sp.
 OS Chimeric - Escherichia coli.
 OS Chimeric - Baculovirus.
 OS Chimeric - Cytomegalovirus.
 OS Chimeric - Rhesus macaque polyoma virus.
 OS Chimeric - Photinus sp.
 OS Chimeric - Salmonella typhimurium.
 OS Chimeric - Homo sapiens.
 FH Key Location/Qualifiers
 FT misc_feature 361..363
 FT /tag= a
 FT /note= *these bases represent nucleotides missing
 FT from the sequence given in the
 FT specification. They are included to
 FT maintain the nucleotide numbering in the

phosphotransferase (neo) gene sequences, in a pBR-derived backbone, and also an anti-B cell antigen CD20 chimeric antibody C2B8 gene. The invention provides a novel method for integrating a desired exogenous DNA at a target site within the genome of a mammalian cell via homologous recombination. This involves transfecting the cell with a 'marker plasmid' such as Desmond (see V61792), which contains a unique sequence that is foreign to the mammalian cell genome and which provides a substrate for homologous recombination, followed by transfection with a 'target plasmid', such as Molly or Mandy (see V61794), containing a sequence which provides for homologous recombination with the unique sequences contained in the marker plasmid, and further comprising a desired DNA that is to be integrated into the mammalian cells, typically an immunoglobulin or other secreted mammalian glycoprotein. The homologous recombination system utilizes the neo gene as a dominant selectable marker. The neo gene is split into 3 exons. Exon 3 is present on the marker plasmid and becomes integrated into the host cell genome upon integration of the marker plasmid into the mammalian cells. Exons 1 and 2 are present on the targeting plasmid, and are separated by an intron into which at least one gene of interest is cloned. Homologous recombination of the targeting vector with the integrated marking vector results in correct splicing of all 3 exons of the neo gene and expression of a functional neo protein. The method is applicable to all mammalian cells, and can be used to express any type of recombinant protein. The use of a triply spliced selectable marker means that all selected colonies arise from homologous recombination. In addition, the number of colonies that need to be screened to identify high producer clones is reduced. An amplifiable gene can be inserted on integration of the marking vector, so that when a gene is targeted to this site, the gene is further enhanced by gene amplification.

Query Match 63.5%; Score 476; DB 1; Length 19001;
Best Local Similarity 78.2%; Pred. No. 3.9e-109;
Matches 585; Conservative 0; Mismatches 160; Indels 3; Gaps 1;
QY 1 ATGAAGTGGAGCTGGGTATTCTCTCTCTGTGACAGTGGCGGCTCCACTCCCAA 60
DB 9426 ATGGGTTGGAGCCCTCATCTTGTCTCTCTCTGTGACAGTGGCGGCTCCACTCCCAA 9485
QY 61 GTCCAACTGTGCAATCCGGCGCGGAGGTCAAGAGCCAGGCGGCTCAGTCAAAAGTGTC 120
DB 9486 GTACAACTGCAGCAGCTGGGGCTGAGCTGTGAAGCTTGGGGCTCAGTGAAGATGTC 9545
QY 121 TGTAAAGCTAGCGGCTATATTTTCTCTTAATTTGGAFTCAATGGTGGCTCAGGCCCC 180
DB 9546 TGCAAGGCTTCTGGCTACACATTTACCAGTTACAATATGCATGGGTAAACAGACACT 9605
QY 181 GGCAGGCGCTGGATGGATGGGTGAGATCTTACCGGGCTCTGGTAGCACCGAATATACC 240
DB 9606 GGTGGGGCTGGAAATGGATGGAGCTATTATCCGGAAATGGTATCTCTCTACAAAT 9665
QY 241 GAAATTTTAAAGACCGCTGTACTATGACGGTGACACTTCGACTAGTACAGTATACATG 300
DB 9666 CAGAGTTCAAGAGCAGGCGCACATTTGACTGCACACAAATCTCCAGCAGCCTACATG 9725
QY 301 GAGCTCTCCAGCCTGCGATCGGAGACACGCGCTCTATTATTGCGCGGCTATTTTTT 360
DB 9726 CAGCTCAGCAGCCTGACATCTGAGGACTCTCGGCTCTATTACTGTGCAAGATCGACTT 9783
QY 361 GGTCTAGCCCGAATTTGGTATTTTGTATTTGGGGTCAAGGAACCTGGTCTACTGTCG 420
DB 9784 -ACTACGGCGGTGACTGTACTTCAATGTCTGGGGCGGAGGACCGGTACCCGTCTCT 9842
QY 421 AGCGCTCCACAGGCGCCCATCGTCTTCCCTGGCGGCTCTCTCCAAAGACACTCT 480
DB 9843 GCAGTAGCACCAGGCGCCCATCGTCTTCCCTGGCACCCCTCTCTCCAGAGACCTCT 9902
QY 481 GGGGGCAGCGGCCCTGGGCTGGCTGGTCAAGGACTACTTCCCGGAACCGGTGACGGTG 540
DB 9903 GGGGGCAGCGGCCCTGGGCTGGCTGGTCAAGGACTACTTCCCGGAACCGGTGACGGTG 9962

QY 541 TCGTGGAACTCAGGCGCCTGACACAGCGCGTGCACACCTTCCCGGCTGTCTCTACAGTCC 600
DB 9963 TCGTGGAACTCAGGCGCCTGACACAGCGCGTGCACACCTTCCCGGCTGTCTCTACAGTCC 10022
QY 601 TCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGGCCCTCCAGCAGCTTGGGACCCAG 660
DB 10023 TCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGGCCCTCCAGCAGCTTGGGACCCAG 10082
QY 661 ACCTACATCTGCAAGCTGAATCACAAGCCAGCACCAACCAAGGTGGACAAAGATTGAG 720
DB 10083 ACCTACATCTGCAAGCTGAATCACAAGCCAGCACCAACCAAGGTGGACAAAGATTGAG 10142
QY 721 CCCAAATCTTGTGACAAAACCTCACACAT 748
DB 10143 CCCAAATCTTGTGACAAAACCTCACACAT 10170

Search completed: September 12, 2000, 21:01:34
Job time: 3603 sec

1

2

3

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 12, 2000, 20:37:50 ; Search time 56.72 Seconds
(without alignments)
1818.880 Million cell updates/sec

Title: US-08-487-283a-12

Perfect score: 750
Sequence: 1 ATGAAGTGGAGCTGGGTAT.....GTGACAAACTGCACATTA 750

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 243080 seqs, 68777915 residues

Total number of hits satisfying chosen parameters: 486160

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_NA: *
1: /cgnl_7/prodata/1/ina/5A_COMB.seq: *
2: /cgnl_7/prodata/1/ina/5B_COMB.seq: *
3: /cgnl_7/prodata/1/ina/5C_COMB.seq: *
4: /cgnl_7/prodata/1/ina/5D_COMB.seq: *
5: /cgnl_7/prodata/1/ina/6_COMB.seq: *
6: /cgnl_7/prodata/1/ina/PCTUS_COMB.seq: *
7: /cgnl_7/prodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	495.2	66.0	8120	5 US-09-027-449-68	Sequence 68, Appl
2	488	65.1	800	5 US-09-027-449-69	Sequence 69, Appl
3	488	65.1	927	5 US-09-027-449-59	Sequence 59, Appl
4	488	65.1	6563	5 US-09-027-449-61	Sequence 61, Appl
5	478.2	63.8	1617	3 US-08-378-939-9	Sequence 9, Appl
6	476	63.5	9209	2 US-08-149-099C-3	Sequence 3, Appl
7	476	63.5	9209	2 US-08-476-275-2	Sequence 2, Appl
8	476	63.5	9209	3 US-08-478-967A-3	Sequence 3, Appl
9	476	63.5	18986	3 US-08-819-866-2	Sequence 2, Appl
10	476	63.5	18986	4 US-09-023-715-2	Sequence 2, Appl
11	467.4	62.3	3282	1 US-08-276-852-154	Sequence 154, App
12	467.4	62.3	3282	1 US-08-276-852-169	Sequence 169, App
13	467.4	62.3	3282	2 US-08-899-575-154	Sequence 154, App
14	467.4	62.3	3282	2 US-08-899-575-169	Sequence 169, App
15	467.4	62.3	3282	2 US-08-899-575-154	Sequence 154, App
16	467.4	62.3	3282	2 US-08-899-575-169	Sequence 169, App
17	467.4	62.3	3282	6 PCT-US95-08743-154	Sequence 154, App
18	467.4	62.3	3282	6 PCT-US95-08743-169	Sequence 169, App
19	467.4	62.3	13254	1 US-08-276-852-156	Sequence 156, App
20	467.4	62.3	13254	2 US-08-276-852-170	Sequence 170, App
21	467.4	62.3	13254	2 US-08-899-575-156	Sequence 156, App
22	467.4	62.3	13254	2 US-08-899-575-170	Sequence 170, App
23	467.4	62.3	13254	2 US-08-899-575-156	Sequence 156, App
24	467.4	62.3	13254	2 US-08-899-575-170	Sequence 170, App
25	467.4	62.3	13254	6 PCT-US95-08743-156	Sequence 156, App
26	467.4	62.3	13254	6 PCT-US95-08743-170	Sequence 170, App

27	459.6	61.3	762	1 US-08-398-613A-57	Sequence 57, Appl
28	459.6	61.3	762	2 US-08-398-612A-57	Sequence 57, Appl
29	459.6	61.3	762	1 US-08-398-611A-57	Sequence 57, Appl
30	459.6	61.3	762	2 US-08-398-611A-57	Sequence 57, Appl
31	459.6	61.3	762	3 US-08-491-334A-57	Sequence 57, Appl
32	459.6	61.3	762	5 US-09-027-449-43	Sequence 43, Appl
33	453.8	60.5	2178	2 US-08-463-587A-24	Sequence 24, Appl
34	453.8	60.5	2178	3 US-08-463-587A-2	Sequence 2, Appl
35	453.8	60.5	2178	6 US-08-923-854-24	Sequence 24, Appl
36	453.8	60.5	2178	6 PCT-US91-09133-25	Sequence 25, Appl
37	443.2	59.1	687	1 US-08-300-386A-1	Sequence 1, Appl
38	443.2	59.1	687	6 PCT-US94-01258-1	Sequence 1, Appl
39	443.2	59.1	687	6 PCT-US95-11235-1	Sequence 1, Appl
40	442.2	59.0	6557	1 US-08-286-740-3	Sequence 3, Appl
41	442.2	59.0	6557	6 PCT-US95-09576-3	Sequence 3, Appl
42	434.4	57.9	11528	5 US-08-444-644-18	Sequence 18, Appl
43	432.8	57.7	756	1 US-08-398-613A-29	Sequence 29, Appl
44	432.8	57.7	756	1 US-08-398-612A-29	Sequence 29, Appl
45	432.8	57.7	756	2 US-08-398-611A-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-09-027-449-68
Sequence 68, Application US/09027449
Patent No. 6025158
GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,449
FILING DATE: 20-Feb-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/038,664
FILING DATE: 21-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P108583-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 8120 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-09-027-449-68

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/027,449
;; FILING DATE: 20-Feb-1998
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/074,330
;; FILING DATE: 22-Jan-1998
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/038,664
;; FILING DATE: 21-Feb-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Love, Richard B.
;; REGISTRATION NUMBER: 34,659
;; REFERENCE/DOCKET NUMBER: P1085R3-2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650/225-5530
;; TELEFAX: 650/952-9881
;; INFORMATION FOR SEQ ID NO: 61:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 6563 base pairs
;; TYPE: Nucleic Acid
;; STRANDEDNESS: Single
;; TOPOLOGY: Linear
;; US-09-027-449-61

Query Match 65.1%; Score 488; DB 5; Length 6563;
Best Local Similarity 79.4%; Pred. No. 4e-118;
Matches 578; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

QY 21 TCTTCTCTCTGTCAGTAACCTGCGGCTCCACTCCCAAGTCCCAACTGGTGCATCCGG 80
DB 1281 TATGTTCTGTTTTTCTATTGCTACAAAGCGGTACGCTAGGTTACGCTAGTGCAGTCTGG 1340

QY 81 CGCGAGGTCAGAAAGCAGGCGCTCAGTCAAGTGTCTGTAAAGCTAGCGGCTATAT 140
DB 1341 CGGTGGCTGGTGCAGCAGGCGCTACTCCGTTTGTCTGTGAGCTTCTGGCTACTC 1400

QY 141 TTTTCTCAATTATTGGATTCAATGGTGCCTCAGCGCCCGGCGGCGGCTGGAATGAT 200
DB 1401 CTCTCGAGTCACTATATGACTGGTGGTCCGTCAGCGCCCGGTAAGGCGCTGGAATGGT 1460

QY 201 GGTGTAGATCTTACCGGGCTCTGTAGCAGCAATATACCGAAATTTTAAAGACCGTGT 260
DB 1461 TGGATATATGATCTTCCATGTGAACTACGTATATCAAAAGTTCAGGGCGGTTT 1520

QY 261 TACTATGAGCGGTGACACTTTCGCTAGTACATGATGAGTCTTCCAGCTCGCATC 320
DB 1521 CACTTATCTCGCAGCAACTCCAAAACACAGCATACCTGCAGATGAACAGCGCTGCGTGC 1580

QY 321 GGAGGACAGCGGCTCTATTATTGGCGGCTTATTTTGTGTTCTAGCCGCAATTGGTA 380
DB 1581 TGAGGACTGCGGCTCTATTACTGTGAAGAGGGGATTATCGCTACAATGTTGACTGGTT 1640

QY 381 TTTTGATGTTTGGGGTCAAGGAACCTGGTCACTGTCTCGAGCGCTCCACCAAGGGCCC 440
DB 1641 CTTCGAGCTTGGGGTCAAGGAACCTGGTCACTGTCTCGGCTCCACCAAGGGCCC 1700

QY 441 ATCGGTCTTCCCTGGCGGCTCTCTCCAGAGCACTCTGGGGGCACAGCGGCTGGG 500
DB 1701 ATCGGTCTTCCCTGGCACCTCTCTCCAGAGCACTCTGGGGGCACAGCGGCTGGG 1760

QY 501 CTGCTGTGTAAGACTACTTCCCGAACCGGTGAGGTGTCTGGAACTCAGGGCGGCT 560
DB 1761 CTGCTGTGTAAGACTACTTCCCGAACCGGTGAGGTGTCTGGAACTCAGGGCGGCT 1820

QY 561 GACCAGCGGCTGCACACTTTCGCGGTGTCTACAGTCTCAGGACTCTACTCCCTCAG 620
DB 1821 GACCAGCGGCTGCACACTTTCGCGGTGTCTACAGTCTCAGGACTCTACTCCCTCAG 1880

QY 621 CAGCGTGTGACCTGGCCCTCTCAGCAGCTTGGGCACCCAGACTTATCTGCAAGCTGAA 680
DB 1881 CAGCGTGTGACCTGGCCCTCTCAGCAGCTTGGGCACCCAGACTTATCTGCAAGCTGAA 1940

QY 681 TCACAGCCCGCAGCAACACACAGGTGGACAAGAGTTGAGCCCAATCTTGTCAAAAAC 740
DB 1941 TCACAGCCCGCAGCAACACACAGGTGGACAAGAGTTGAGCCCAATCTTGTGACAAAAC 2000

QY 741 TCACACAT 748
DB 2001 TCACACAT 2008

RESULT 5
US-08-378-939-9
; Sequence 9, Application US/08378939
; Patent No. 5876961
; GENERAL INFORMATION:
; APPLICANT: CROWE, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
; STREET: 555 THIRTEENTH ST. N.W.
; CITY: WASHINGTON
; STATE: D. C.
; COUNTRY: U.S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,939
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/952640
; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1808-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1617 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 35..92
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 93..1465
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 35..1465
; US-08-378-939-9

Query Match 63.8%; Score 478.2; DB 3; Length 1617;
Best Local Similarity 78.0%; Pred. No. 9.4e-116;
Matches 595; Conservative 0; Mismatches 153; Indels 15; Gaps 1;

QY 1 ATGAAGTGGAGCTGGGTTATCTCTCTCTCTAGTAACAGTCCGCGCTCCACTCCCAA 60
DB 35 ATGGACTGGACCTGGAGGTTCTCTTGTGTTGGCAGCAGCTACAGTGTCCAGTCCCAG 94

NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,967A
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
APPLICATION NUMBER: US 07/978,891
FILING DATE: 12-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-014
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 9209 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOHETICAL: NO
ANTI-SENSE: NO
US-08-478-967A-3

Query Match 63.5%; Score 476; DB 3; Length 9209;
Best Local Similarity 78.2%; Pred. No. 5.9e-115;
Matches 585; Conservative 0; Mismatches 160; Indels 3; Gaps 1;
QY 1 ATGAAGTGGAGCTGGTATTCTTCTCTCTGACGTAAGTCCGGGCTCCACTCCCA 60
DB 2401 ATGGGTGGAGCCCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2460
QY 61 GTCCAACTGGGCAATCGCGCGCGAGGTCAAGAACCGAGGCGCTCAAGTATGCC 120
DB 2461 GTCAACTGAGCAGCCTGGGGCTGAGCTGTGAAGCCTGGGGCTCAAGTATGCC 2520
QY 121 TGTAACTAGAGCGCTATTTTCTTATATGATGATTCAATGGGCTCGTCAAGCC 180
DB 2521 TCGAAGCTTCTGCTACATATTACAGTTACATATGCACTGGTAAACAGCACT 2580
QY 181 GGGCAGGCGCTGGAATGATGGTGAATCTTACCAGGCGCTGTAGACCGAATATAC 240
DB 2581 GGTGGGCGCTGGAATGATGGTGAATCTTATCCCGAATGGTGAATATCTTCAAT 2640
QY 241 GAAATTTTAAAGCAGCTGTACTATGACGGGTGACACTTGCATGACATATATG 300
DB 2641 CAGAAATTTCAAGCAGGCGCACATGCTCAGCAATCTCTCAGACAGCCATAC 2700
QY 301 GAGCTTCAGCGCTGAGATGAGACAGCGCGCTATTTATGCGCGCTATTTT 360
DB 2701 CAGCTCAGCAGCTGAGATGAGACAGCGCGCTATTTATGCGCGCTATTTT 2758
QY 361 GGTCTAGCCGATGATTTTGTATGTTGGGTCAAGAACCGTGTCACTCTCG 420
DB 2759 -ACTACGGCGGTGACTGTACTCAATGTCTGGGCGCAGGAGCAGGTACCGTCTCT 2817

QY 421 AGCGCTCCACCAAGGCGCCATCGCTTCCCTTGGCGCCCTCTCTCAAGACACTCT 480
DB 2818 GCAGTAGACCAAGGCGCCATCGCTTCCCTTGGCGCCCTCTCTCAAGACACTCT 2877
QY 481 GGGGCGACAGCGCCCTTGGGCTGCTGTGCAAGGACTTCTCCCGAACCCTGACGG 540
DB 2878 GGGGCGACAGCGCCCTTGGGCTGCTGTGCAAGGACTTCTCCCGAACCCTGACGG 2937
QY 541 TCGTGAATCAGGCGCCCTGACAGCGCGCTGACACACTTCCCGGCTCTCTACAGTCC 600
DB 2938 TCGTGAATCAGGCGCCCTGACAGCGCGCTGACACACTTCCCGGCTCTCTACAGTCC 2997
QY 601 TCAGGACTCTACTCCCTGACAGCGGTGTGACCGTCCCTCCAGCAGCTTGGGCAACCG 660
DB 2998 TCAGGACTCTACTCCCTGACAGCGGTGTGACCGTCCCTCCAGCAGCTTGGGCAACCG 3057
QY 661 ACCTACATCTGCAAGTGAATCAAGACCCACCAACCAAGTGGACAAAGATTGAG 720
DB 3058 ACCTACATCTGCAAGTGAATCAAGACCCACCAACCAAGTGGACAAAGATTGAG 3117
QY 721 CCCAATCTGTGACAAATCCACAT 748
DB 3118 CCCAATCTGTGACAAATCCACAT 3145

RESULT 9
US-08-819-866-2
Sequence 2, Application US/08819866
Patent No. 5830698
GENERAL INFORMATION:
APPLICANT: REFF, Mitchell E.
APPLICANT: BARNETT, Richard Spence
APPLICANT: McLACHLAN, Karen Retta
TITLE OF INVENTION: NOVEL METHOD FOR INTEGRATING GENES AT
SPECIFIC SITES IN MAMMALIAN CELLS VIA HOMOLOGOUS
RECOMBINATION AND VECTORS FOR ACCOMPLISHING THE SAME
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,866
FILING DATE: 14-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-352
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18986 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-819-866-2

Query Match 63.5%; Score 476; DB 3; Length 18986;
Best Local Similarity 78.2%; Pred. No. 7.3e-115;
Matches 585; Conservative 0; Mismatches 160; Indels 3; Gaps 1;

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QY 1 ATGAAGTGAGCTGGGTTATTCTCTCTCTGTCACTAAGTGGGGTCCACTCCCAA 60
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Db 9433 ATGGTTGGAGCCTCATCTTCCTCTCTCTGTGTGTAGCGGTCTGTGCCAG 9492
    ||| ||||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 GTCCAACTGGTGAATCCGGCCGAGGTCAAGAGCCAGGGGCTCAGTCAAAAGTGTC 120
    ||| ||||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 9493 GTACAACTGCAGCCTGGGGCTGAGCTGTGAAGCCTGGGCTCAGTGAAGATGTC 9552
    ||| ||||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 TGTAACTAGCGCTATATTTTCTTAATTTGATTTCAATGGGTGCGTCAGGCCCC 180
    ||| ||||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 9553 TGAAGGCTTCTGCTACACATTTACCAGTTTACAAATATGCTGGTAAACACAGACCT 9612
    ||| ||||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 GGCAGGCTGGAATGGATGGGTGAGATCTACCGGCTCTGTGAGCACCAATATACC 240
    ||| ||||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 9613 GGTGGGCTGGAATGGATGGGTGAGATCTACCGGCTCTGTGAGCACCAATATACC 9672
    ||| ||||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 241 GAAATTTTAAAGACCGCTTACTATGACGCGTGACACTTCGACTAGTACATATACATG 300
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Db 9673 CAGAAGTTCAAAGCAAGGCCACATTGACTGCAGACAAATCCTCCAGCACAGCTACATG 9732
    ||| ||||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 301 GAGCTTCCAGCTGCGATCGGAGACACGCGCTCTATATGCGCGCTATTTTTCCT 360
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Db 9733 CAGCTACAGCCTGACATCTGAGGACTCTGCGGTCTATTCTGTCAAGATCGACTT-- 9790
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QY 361 GGTTCATGCCGAATTTGATTTTGGGTCAAGGAACCTGTGCTACTGTCTCG 420
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Db 9791 -ACTAGCGGTGACTGTGACTTCAATGCTGGGCGGAGGACCCAGCTCACCCTCTCT 9849
    ||| ||||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 421 AGCGCTCCACCAAGGCCCTCGGTCTTCCCGTGGCGCCCTCTCCCAAGACACCTCT 480
    ||| ||||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 9850 GCAGTAGACCAAGGCCCTCGGTCTTCCCGTGGCGCCCTCTCCCAAGACACCTCT 9909
    ||| ||||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 481 GGGGCGACAGCGCCCTGGGCTGCGCTCAAGGACTCTCCCGAACCGGTGACGGTG 540
    ||| ||||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 9910 GGGGCGACAGCGCCCTGGGCTGCGCTCAAGGACTCTCCCGAACCGGTGACGGTG 9969
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QY 541 TCGTGGAACTCAGCGGCTGACAGCGGCTGACACCTTCCCGGCTGCTCTACAGTCC 600
    ||| ||||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 9970 TCGTGGAACTCAGCGGCTGACAGCGGCTGACACCTTCCCGGCTGCTCTACAGTCC 10029
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```

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RESULT 10
US-09-023-715-2
; Sequence 2, Application US/09023715
; Patent No. 5998144
; GENERAL INFORMATION:
; APPLICANT: REFF, Mitchell E.
; APPLICANT: BARNETT, Richard Spence
; APPLICANT: MCLACHLAN, Karen Retta
; TITLE OF INVENTION: NOVEL METHOD FOR INTEGRATING GENES AT
; SPECIFIC SITES IN MAMMALIAN CELLS VIA HOMOLOGOUS
; RECOMBINATION AND VECTORS FOR ACCOMPLISHING THE SAME
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
```

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023/715
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/819,866
; FILING DATE: 14-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-352
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18986 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-023-715-2
```

```
Query Match 63.5%; Score 476; DB 4; Length 18986;
Best Local Similarity 78.2%; Pred. No. 7, 3e-115;
Matches 585; Conservative 0; Mismatches 160; Indels 3; Gaps 1;

QY 1 ATGAAGTGAGCTGGGTTATTCTCTCTCTGTCACTAAGTGGGGTCCACTCCCAA 60
    ||| ||||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 9433 ATGGTTGGAGCCTCATCTTCCTCTCTGTGTGTAGCGGTCTGTGCCAG 9492
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QY 61 GTCCAACTGGTGAATCCGGCCGAGGTCAAGAGCCAGGGGCTCAGTCAAAAGTGTC 120
    ||| ||||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 9493 GTACAACTGCAGCCTGGGGCTGAGCTGTGAAGCCTGGGCTCAGTGAAGATGTC 9552
    ||| ||||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 TGTAAAGCTAGCGGCTATATTTTCTTAATTTGATTTCAATGGGTGCGTCAGGCCCC 180
    ||| ||||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 9553 TGAAGGCTTCTGCTACACATTTACCAGTTTACAAATATGCTGGTAAACACAGACCT 9612
    ||| ||||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 GGCAGGCGCTGGAATGGATGGGTGAGATCTTACCGGCTCTGTGAGCACCAATATACC 240
    ||| ||||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 9613 GGTGGGCTGGAATGGATGGGTGAGATCTTATCCCGGAAATGGTGTACTCTTCAAT 9672
    ||| ||||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 241 GAAATTTTAAAGACCGCTTACTATGACGCGTGACACTTCGACTAGTACATATACATG 300
    ||| ||||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 9673 CAGAAGTTCAAAGCAAGGCCACATTGACTGCAGACAAATCCTCCAGCACAGCTACATG 9732
    ||| ||||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 301 GAGCTTCCAGCTGCGATCGGAGACACGCGCTCTATATGCGCGCTATTTTTCCT 360
    ||| ||||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 9733 CAGCTACAGCCTGACATCTGAGGACTCTGCGGTCTATTCTGTCAAGATCGACTT-- 9790
    ||| ||||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 361 GGTTCATGCCGAATTTGATTTTGGGTCAAGGAACCTGTGCTACTGTCTCG 420
    ||| ||||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 9791 -ACTAGCGGTGACTGTGACTTCAATGCTGGGCGGAGGACCCAGCTCACCCTCTCT 9849
    ||| ||||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 421 AGCGCTCCACCAAGGCCCTCGGTCTTCCCGTGGCGCCCTCTCCCAAGACACCTCT 480
    ||| ||||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 9850 GCAGTAGACCAAGGCCCTCGGTCTTCCCGTGGCGCCCTCTCCCAAGACACCTCT 9909
    ||| ||||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 481 GGGGCGACAGCGCCCTGGGCTGCGCTCAAGGACTCTCCCGAACCGGTGACGGTG 540
    ||| ||||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 9910 GGGGCGACAGCGCCCTGGGCTGCGCTCAAGGACTCTCCCGAACCGGTGACGGTG 9969
    ||| ||||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 541 TCGTGGAACTCAGCGGCTGACAGCGGCTGACACCTTCCCGGCTGCTCTACAGTCC 600
    ||| ||||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 9970 TCGTGGAACTCAGCGGCTGACAGCGGCTGACACCTTCCCGGCTGCTCTACAGTCC 10029
    ||| ||||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```


Best Local Similarity 78.7%; Pred. No. 7.5e-113;
Matches 577; Conservative 0; Mismatches 141; Indels 15; Gaps 1;

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QY 1 ATGAGTGGAGCTGGGATTTCTCTCTCCCTGAGTAACTGCGGCGCTCCACCCAA 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 15 ATGAGATGAGCTGGGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCA 74
QY 61 GTCCAACTGTGCAATCCGGCGCCAGGTCAAGAACCGGGGCTCACTCAAGTGTCC 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 75 GTTCAGCTGTTCAGTCCGGGCTGAGGAGTGAAGACCTGGGGCTCACTGAAGTTCT 134
QY 121 TGTAAAGCTAGCGGTATATTTTCTATTTATTTGATTCATGGGTGGCTGAGCC 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 135 TGTGAGGCTTGTGATTAAGATTAAGTAACTTTGATTTATTTGATTTGGTGG 194
QY 181 GGGCAGGCGCTGAGTGGATGGGTGAGATCTTACCGGGCTGTGTAGACCGAATATAC 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 195 GGACAGAGGTTGAGTGGATGGATGATGATCAATCCTTACACGGAACAAAGATTTTCA 254
QY 241 GAAATTTTAAAGACCGTGTACTATGACGCGTACCTTCACTAGTACATATACATG 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 255 GCGAAGTTCACAGAGATGATCACTTTACCGGGACACATCCGGCAACACAGCTACATG 314
QY 301 GAGCTCTCAGCTGCGATCGAGAGACAGCGGCTCTATTTATTTGCGCG----- 348
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 315 GAGTTGAGAGACCTCAGGCTCTGCAACAGCGGCTGTATTTATTTGCGAGAGTGGG 374
QY 349 ---CGTTATTTTGTGTTCTTACGCCGAATGGTATTTGATTTGGGTGCAAGAAC 405
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 375 TATAGTTGGATGATTTCTCCAGACAAATTTATATGAGAGTCTGGGCAAGGAAACC 434
QY 406 CTGCTACATGCTCTGAGCGGCTCCACCAAGGGCCATCGGTCTCCCGCTGGCGCTCC 465
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 435 ACGGTCACTGAGAGTCACTTCCACCAAGGGCCATCGGTCTCCCGCTGGCGCTCC 494
QY 466 TCCAAGAGCACCTTGGGGGACAGCGGCGCTGGGCTGCTGCTCAAGGACTACTTCCC 525
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 495 TCCAAGAGCACCTTGGGGGACAGCGGCGCTGGGCTGCTGCTCAAGGACTACTTCCC 554
QY 526 GAACCGGAGAGGTCTCTGGAATCTCAGGCGCTGACAGCGGGGTGCAACCTTCCC 585
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 555 GAACCGGAGAGGTCTCTGGAATCTCAGGCGCTGACAGCGGGGTGCAACCTTCCC 614
QY 586 GCTGCTCAGAGCTCTGAGACTACTTCCCTCAGCAGGGTGGTGGCTGCTCCAC 645
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 615 GCTGCTCAGAGCTCTGAGACTACTTCCCTCAGCAGGGTGGTGGCTGCTCCAC 674
QY 646 AGCTTGGGACCCAGACCTTACATCTGCAAGGTGAATCAACCCAGCAACCAAGTGT 705
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 675 AGCTTGGGACCCAGACCTTACATCTGCAAGGTGAATCAACCCAGCAACCAAGTGT 734
QY 706 GACAAGAAAGTTG 718
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Db 735 GACAAGAAAGTTG 747

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RESULT 14
US-08-899-575-169/c
Sequence 169, Application US/08899575
Patent No. 5770440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Bairds, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESSES:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla

```

STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 169:
SEQUENCE CHARACTERISTICS:
LENGTH: 3282 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-899-575-169

```

Query Match 62.3%; Score 467.4; DB 2; Length 3282;
Best Local Similarity 78.7%; Pred. No. 7.5e-113;

Matches 577; Conservative 0; Mismatches 141; Indels 15; Gaps 1;

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QY 1 ATGAGTGGAGCTGGGATTTCTCTCTCCCTGAGTAACTGCGGCGCTCCACCCAA 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3268 ATGAGATGAGCTGGGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCA 3209
QY 61 GTCCAACTGTGCAATCCGGCGCCAGGTCAAGAACCGGGGCTCACTCAAGTGTCC 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3208 GTTCAGCTGTTCAGTCCGGGCTGAGGAGTGAAGACCTGGGGCTCAGAGAGTTCT 3149
QY 121 TGTAAAGCTAGCGGTATATTTTCTATTTATTTGATTCATGGGTGGCTGAGCC 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3148 TGTGAGGCTTGTGATTAAGATTAAGTAACTTTGATTTATTTGATTTGGTGG 3089
QY 181 GGGCAGGCGCTGAGTGGATGGGTGAGATCTTACCGGGCTGTGTAGACCGAATATAC 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3088 GGCACAGAGTTGAGTGGATGGATGATCAATCCTTACACGGAACAAAGATTTTCA 3029
QY 241 GAAATTTTAAAGACCGTGTACTATGACGCGTACACTTGAATGATACATATACATG 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3028 GCGAAGTTCACAGAGATGATCACTTTACCGGGACACATCCGGAACAGCTACATG 2969
QY 301 GAGCTCTCAGCTGCGATCGAGAGACAGCGGCTCTATTTATTTGCGCG----- 348
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2968 GAGTTAGAGAGCTTCAAGCTCTGCAACAGCGGCTGTATTTATTTGCGAGTGG 2909
QY 349 ---CGTTATTTTGTGTTCTTACGCCGAATGGTATTTGATTTGGGTGCAAGAAC 405
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2908 TATAGTTGGATGATTTCTCCAGGACAAATTTATATGAGAGCTTGGGCAAGAAC 2849
QY 406 CTGCTACATGCTCTGAGCGGCTCCACCAAGGGCCATCGGTCTCCCGCTGGCGCTCC 465
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2848 ACGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2789

```


5/7/18 (Item 18 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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06105444 BIOSIS NO.: 000085068593
PREPARATION AND CHARACTERIZATION OF MONOCLONAL ANTIBODIES AGAINST THE FIFTH
COMPONENT OF RABBIT COMPLEMENT C5
AUTHOR: GICLAS P C; BAKER S L; GILLESPIE M L; WILCOX C
AUTHOR ADDRESS: DEP. PEDIATR., NATL. JEW. CENT. IMMUNOL. RESPIR. MED., 1400
JACKSON ST., DENVER, COLO. 80206, USA.
JOURNAL: J IMMUNOL METHODS 105 (2). 1987. 201-210.
FULL JOURNAL NAME: Journal of Immunological Methods
CODEN: JIMMB
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: By immunizing mice genetically deficient in C5 we were able to obtain a group of monoclonal antibodies to rabbit C5 that cross-react with C5 from a wide variety of mammalian sera, including mouse. The specificity of the monoclonal **antibodies** was against native C5 and C5b but not C5a. The **antibodies** strongly inhibit the expression of C5 hemolytic activity. We suggest that these monoclonal **antibodies** will be useful for studying C5 as well as providing a way to selectively deplete C5 from plasma in vitro or in vivo.